



SEQUENCE LISTING

<10> Council of Scientific and Industrial Research

<120> A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE
PROTEINS USEFUL AS ANTI-INFECTIVES

<130> Q63915

<160> 118

<170> PatentIn version 3.2

<210> 1

<211> 51

<212> PRT

<213> C. jejuni

<220>

<221> misc_feature

<223> highly acidic protein

<220>

<221> misc_feature

<223> gi|6967728

<400> 1

Met Ala Tyr Glu Asp Glu Glu Asp Leu Asn Tyr Asp Asp Tyr Glu Asn
1 5 10 15

Glu Asp Glu Glu Tyr Pro Gln Asn His His Lys Asn Tyr Asn Tyr Asp
20 25 30

Asp Asp Asp Tyr Glu Tyr Asp Asp Asp Asn Asn Asp Asp Asp Phe Tyr
35 40 45

Glu Met Asp
50

<210> 2

<211> 32

<212> PRT

<213> C. jejuni

<220>

<221> misc_feature

<223> small hydrophobic protein

<220>

<221> misc_feature

<223> gi|6969129

<400> 2

Met Thr Met Leu Asp Ile Phe Glu Ile Ile Phe Ile Thr Thr Val Val
1 5 10 15

Ile Ile Gly Phe Gly Gly Ile Val Phe Val Val Thr Lys Glu Lys Lys
20 25 30

<210> 3
<211> 57
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> putative coiled coil protein

<220>
<221> misc_feature
<223> gi|6968493

<400> 3

Met Ser Phe Glu Glu Asn Leu Lys His Ala Asn Glu Ser Leu Glu Lys
1 5 10 15

Leu Asn Asn Gln Glu Leu Ala Leu Asp Glu Ser Val Lys Ile Tyr Lys
20 25 30

Glu Gly Leu Glu Ser Ile Lys Lys Ala Arg Leu Glu Leu Glu Lys Ala
35 40 45

Lys Leu Glu Val Glu Gln Ile Asp Glu
50 55

<210> 4
<211> 542
<212> PRT
<213> C. jejuni

<220>
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<223> highly acidic protein

<220>
<221> misc_feature
<223> gi|6968611

<400> 4

Met Lys Ile Leu Leu Leu Asn Glu Asn Pro Val Val Ser Arg Leu Val
1 5 10 15

Ser Leu Ser Ala Lys Lys Met Ser Tyr Asp Phe Glu Glu Leu Asn Ala
 20 25 30

Tyr Ser Glu Asn Leu Gly Asn Tyr Asp Val Ile Val Val Asp Ser Asp
 35 40 45

Thr Pro Ala Pro Leu Lys Ile Leu Lys Glu Lys Cys Asp Arg Leu Ile
 50 55 60

Phe Leu Ala Pro Arg Asn Gln Asn Val Glu Asp Ile Asp Ala Gln Ile
 65 70 75 80

Leu Gln Lys Pro Phe Leu Pro Thr Asp Phe Leu Asn Leu Leu Asn Asn
 85 90 95

Lys Asp Ala Asn Lys His Thr Ser Ile Asp Leu Pro Met Leu Ser Asn
 100 105 110

Asp Glu Asn Pro Tyr Ala Asp Ile Ser Leu Asp Leu Asp Asn Leu Asn
 115 120 125

Leu Asp Asp Leu Pro Asp Glu Asn Ser Leu Asp Ile Asn Ser Glu Gly
 130 135 140

Met Glu Asp Leu Ser Phe Asp Asp Asp Ala Gln Asp Asp Asn Ala Asn
 145 150 155 160

Lys Thr Leu Glu Thr Gln Asn Leu Glu His Glu Thr Ile Lys Glu Gln
 165 170 175

Thr Gln Glu Asp Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly
 180 185 190

Glu Ser Glu Lys Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr
 195 200 205

Glu Pro Ser Leu Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu
 210 215 220

Ile Lys Glu Asp Asp Lys Asn Glu Glu Ile Glu Lys Gln Glu Leu Leu
 225 230 235 240

Asp Asp Ser Lys Thr Asn Thr Leu Glu Met Gln Glu Glu Leu Ser Glu
 245 250 255

Ser Gln Asp Asp Asn Ser Asn Lys Thr Leu Glu Thr Gln Asn Leu Glu
260 265 270

His Asp Asn Leu Glu Gln Glu Thr Ile Lys Glu Gln Thr Gln Glu Asp
275 280 285

Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly Glu Ser Glu Lys
290 295 300

Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr Glu Pro Ser Leu
305 310 315 320

Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu Asp Asn Lys Glu
325 330 335

Leu Gln Ala Asn Ile Ser Asp Phe Asp Asp Leu Pro Glu Val Glu Glu
340 345 350

Gln Glu Lys Glu Met Asp Phe Asp Asp Leu Pro Glu Asp Ala Glu Phe
355 360 365

Leu Gly Gln Ala Lys Tyr Asn Glu Glu Ser Glu Glu Asn Leu Glu Glu
370 375 380

Phe Ala Pro Val Val Glu Glu Asp Ile Gln Asp Glu Ile Asp Asp Phe
385 390 395 400

Ala Ser Asn Leu Ser Thr Gln Asp Gln Ile Lys Glu Glu Leu Ala Gln
405 410 415

Leu Asp Glu Leu Asp Tyr Gly Ile Asp Ser Asp Asn Ser Ser Lys Val
420 425 430

Leu Glu Asp Phe Lys Asp Glu Pro Ile Leu Asp Asp Lys Glu Leu Gly
435 440 445

Thr Asn Glu Glu Glu Val Val Val Pro Asn Leu Asn Ile Ser Asp Phe
450 455 460

Asp Thr Leu Lys Glu Ser Asp Ile Gln Glu Ala Leu Gly Glu Glu Ile
465 470 475 480

Leu Glu Lys Asn Glu Glu Pro Ile Val Ser Asp Val Thr Lys Asp Asp
485 490 495

Asn Ser Glu Glu Ile Val Asn Glu Leu Ser Gln Ser Ile Ala Gly Ala
500 505 510

Ile Thr Ser Ser Ile Lys Asp Asp Thr Leu Lys Ala Ala Leu Lys Gly
515 520 525

Met Asn Met Asn Ile Asn Ile Asn Ile Ser Phe Lys Glu Asp
530 535 540

<210> 5
<211> 172
<212> PRT
<213> C. pneumoniaeCWL029

<220>
<221> misc_feature
<223> histone like protein 2

<220>
<221> misc_feature
<223> gi|4376663

<400> 5

Met Ile Gly Ala Gln Lys Lys Gln Ser Gly Lys Lys Thr Ala Ser Arg
1 5 10 15

Ala Val Arg Lys Pro Ala Lys Lys Val Ala Ala Lys Arg Thr Val Lys
20 25 30

Lys Ala Thr Val Arg Lys Thr Ala Val Lys Lys Pro Ala Val Arg Lys
35 40 45

Thr Ala Ala Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg Thr
50 55 60

Val Arg Lys Thr Val Ala Lys Lys Pro Ala Val Lys Lys Val Ala Ala
65 70 75 80

Lys Arg Val Val Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg
85 90 95

Ala Val Arg Lys Thr Val Ala Lys Lys Pro Val Ala Arg Lys Thr Thr
100 105 110

Val Ala Lys Gly Ser Pro Lys Lys Ala Ala Ala Cys Ala Leu Ala Cys
115 120 125

His Lys Asn His Lys His Thr Ser Ser Cys Lys Arg Val Cys Ser Ser
 130 135 140

Thr Ala Thr Arg Lys His Gly Ser Lys Ser Arg Val Arg Thr Ala His
 145 150 155 160

Gly Trp Arg His Gln Leu Ile Lys Met Met Ser Arg
 165 170

<210> 6
 <211> 63
 <212> PRT
 <213> C. trachomatis

<220>
 <221> misc_feature
 <223> hypothetical protein-possible frameshift with CT593

<220>
 <221> misc_feature
 <223> gi|3522902

<400> 6

Met Phe Thr Leu Phe Leu Cys Glu His Leu Leu Thr Asn Ile Leu Ala
 1 5 10 15

Ser Ser Phe Leu Ala Lys Ser Gln Gly Phe Ile Thr Leu Val Asn Leu
 20 25 30

Phe His Lys Ile Pro Gly Leu Lys Val Ile Glu Ile Thr Cys Leu Ala
 35 40 45

Leu Pro Leu Gly Ile His Ser Ile Ile Gly Phe Ser Tyr Leu Leu
 50 55 60

<210> 7
 <211> 203
 <212> PRT
 <213> C. trachomatis

<220>
 <221> misc_feature
 <223> histone like protein 2

<220>
 <221> misc_feature
 <223> gi|3328438

<400> 7

Met Asn Met Leu Gly Val Gln Lys Lys Cys Ser Thr Arg Lys Thr Ala
 1 5 10 15

Ala Arg Lys Thr Val Val Arg Lys Pro Ala Ala Lys Lys Thr Ala Ala
 20 25 30

Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys Thr Val Ala Arg
 35 40 45

Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys Pro Val Ala Lys
 50 55 60

Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys
 65 70 75 80

Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys
 85 90 95

Pro Val Ala Lys Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Ala
 100 105 110

Val Ala Lys Lys Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val
 115 120 125

Ala Ala Arg Lys Pro Val Ala Lys Arg Val Ala Ser Thr Lys Lys Ser
 130 135 140

Ser Ile Ala Val Lys Ala Gly Val Cys Met Lys Lys His Lys His Thr
 145 150 155 160

Ala Ala Cys Gly Arg Val Ala Ala Ser Gly Val Lys Val Cys Ala Ser
 165 170 175

Ala Ala Lys Arg Lys Thr Asn Pro Asn Arg Ser Arg Thr Ala His Ser
 180 185 190

Trp Arg Gln Gln Leu Met Lys Leu Val Ala Arg
 195 200

<210> 8
 <211> 372
 <212> PRT
 <213> H. influenzae

<220>

<221> misc_feature
<223> outer membrane integrity protein (tolA)

<220>
<221> misc_feature
<223> gi|1573353

<400> 8

Met Gln Asn Asn Arg Gln Lys Lys Gly Ile Asn Ala Phe Ala Ile Ser
1 5 10 15

Ile Leu Leu His Phe Ile Leu Phe Gly Leu Leu Ile Leu Ser Ser Leu
20 25 30

Tyr His Thr Val Glu Ile Met Gly Gly Gly Glu Gly Glu Gly Asp Val
35 40 45

Ile Gly Ala Val Ile Val Asp Thr Gly Thr Ala Ala Gln Glu Trp Gly
50 55 60

Arg Ile Gln Gln Gln Lys Lys Gly Gln Ala Asp Lys Gln Lys Arg Pro
65 70 75 80

Glu Pro Val Val Glu Lys Pro Pro Glu Pro Asn Gln Glu Glu Ile
85 90 95

Lys His Gln Gln Glu Val Gln Arg Gln Glu Glu Leu Lys Arg Gln Gln
100 105 110

Glu Gln Gln Arg Gln Gln Glu Ile Lys Lys Gln Gln Glu Gln Ala Arg
115 120 125

Gln Glu Ala Leu Glu Lys Gln Lys Gln Ala Glu Glu Ala Lys Ala Lys
130 135 140

Gln Ala Ala Glu Ala Ala Lys Leu Lys Ala Asp Ala Glu Ala Lys Arg
145 150 155 160

Leu Ala Ala Ala Ala Lys Gln Ala Glu Glu Glu Ala Lys Ala Lys Ala
165 170 175

Ala Glu Ile Ala Ala Gln Lys Ala Lys Gln Glu Ala Glu Ala Lys Ala
180 185 190

Lys Leu Glu Ala Glu Ala Lys Ala Lys Ala Val Ala Glu Ala Lys Ala
195 200 205

Lys Ala Glu Ala Glu Ala Lys Ala Lys Ala Ala Ala Glu Ala Lys Ala
210 215 220

Lys Ala Asp Ala Glu Ala Lys Ala Ala Thr Glu Ala Lys Arg Lys Ala
225 230 235 240

Asp Gln Ala Ser Leu Asp Asp Phe Leu Asn Gly Gly Asp Ile Gly Gly
245 250 255

Gly Ser Ala Ser Lys Gly Gly Asn Thr Asn Lys Gly Gly Thr Gln Gly
260 265 270

Ser Gly Ala Ala Leu Gly Ser Gly Asp Gly Gly Lys Val Gly Asp Gln
275 280 285

Tyr Ala Gly Val Ile Lys Lys Glu Ile Gln Arg Arg Phe Leu Lys Asp
290 295 300

Pro Asn Phe Ala Gly Lys Val Cys Arg Ile Lys Ile Gln Leu Gly Arg
305 310 315 320

Asp Gly Thr Ile Leu Gly Tyr Gln Lys Ile Ser Gly Ser Asp Asp Ile
325 330 335

Cys Ser Ala Ala Leu Ser Ala Val Ala Arg Thr Lys Lys Val Pro Ala
340 345 350

Ala Pro Ser Asp Glu Ile Tyr Glu Lys Tyr Lys Ser Pro Ile Ile Asp
355 360 365

Phe Asp Ile Arg
370

<210> 9
<211> 538
<212> PRT
<213> H. influenzae

<220>
<221> misc_feature
<223> thiamin ABC transporter, permease protein, putative

<220>
<221> misc_feature
<223> gi|1574049

<400> 9

Met Phe Ser Leu Phe His His Pro Gln Leu Arg Pro Arg His Tyr Ala
 1 5 10 15
 Gly Gly Val Val Val Ile Ser Phe Ile Ile Leu Phe Tyr Gly Gly Ala
 20 25 30
 Leu Ser Ser Ile Phe Ala Leu Gly Gly Glu Leu Gln Trp Arg Ala Trp
 35 40 45
 Phe Thr Asp Asp Tyr Leu Gln His Leu Ile Leu Phe Ser Phe Gly Gln
 50 55 60
 Ala Leu Leu Ser Thr Val Leu Ser Ile Phe Phe Gly Leu Leu Leu Ala
 65 70 75 80
 Arg Ala Leu Phe Tyr Lys Pro Phe Leu Gly Lys Lys Trp Leu Leu Lys
 85 90 95
 Leu Met Ser Leu Thr Phe Val Leu Pro Ala Leu Val Val Ile Phe Gly
 100 105 110
 Leu Ile Gly Ile Tyr Gly Ser Ser Gly Trp Leu Ala Trp Leu Ala Asn
 115 120 125
 Leu Phe Gly Met Ser Trp Gln Gly His Ile Tyr Gly Leu Ser Gly Ile
 130 135 140
 Leu Ile Ala His Leu Phe Phe Asn Ile Pro Leu Ala Ala Gln Leu Phe
 145 150 155 160
 Leu Gln Ser Leu Gln Ser Ile Pro Tyr Gln Gln Arg Gln Leu Ala Ala
 165 170 175
 Gln Leu Asn Leu Gln Gly Trp Gln Phe Val Lys Leu Val Glu Trp Pro
 180 185 190
 Val Phe Arg Gln Gln Cys Leu Pro Thr Phe Ser Leu Ile Phe Met Leu
 195 200 205
 Cys Phe Thr Ser Phe Thr Val Val Leu Thr Leu Gly Gly Gly Pro Gln
 210 215 220
 Tyr Thr Thr Leu Glu Thr Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
 225 230 235 240

Asp Leu Pro Lys Ala Ala Leu Phe Ala Met Leu Gln Phe Val Phe Cys
245 250 255

Leu Ile Leu Phe Ser Leu Thr Ser Arg Phe Ser Leu Ser Asn Gln Asn
260 265 270

Gly Leu Ser Asn Ser Asn Ile Trp Phe Glu Lys Pro Lys Ser Ala Val
275 280 285

Lys Ile Phe His Ile Leu Val Leu Leu Val Phe Val Phe Phe Leu Phe
290 295 300

Ser Pro Val Leu Asn Ile Leu Ile Ser Ala Leu Ser Ser Ser Asn Leu
305 310 315 320

Leu Thr Val Trp His Asn Ser Gln Leu Trp Arg Ala Leu Gly Tyr Ser
325 330 335

Leu Ser Ile Ala Pro Leu Ser Ala Leu Leu Ala Leu Thr Met Ala Ile
340 345 350

Ala Leu Leu Leu Leu Ser Arg Arg Leu Glu Trp Leu His Tyr Gln Lys
355 360 365

Ile Ser Gln Phe Ile Ile Asn Ala Gly Met Val Ile Leu Ala Ile Pro
370 375 380

Ile Leu Val Leu Ala Met Gly Leu Phe Leu Leu Leu Gln Asp Arg Asp
385 390 395 400

Phe Ser Asn Ile Asp Leu Phe Ile Ile Val Val Phe Cys Asn Ala Leu
405 410 415

Ser Ala Met Pro Phe Val Leu Arg Ile Leu Ser Ala Pro Phe His Asn
420 425 430

Asn Met Arg Tyr Tyr Glu Asn Leu Cys Asn Ser Leu Gly Ile Val Gly
435 440 445

Trp Gln Arg Phe Tyr Leu Ile Glu Trp Lys Thr Leu Arg Ala Pro Leu
450 455 460

Arg Tyr Ala Phe Ala Leu Gly Leu Ala Leu Ser Leu Gly Asp Phe Thr
465 470 475 480

Ala Ile Ala Leu Phe Gly Asn Gln Glu Phe Thr Ser Leu Pro His Leu
485 490 495

Leu Tyr Gln Gln Leu Gly Asn Tyr Arg Asn Gln Asp Ala Ala Val Thr
500 505 510

Ala Gly Ile Leu Leu Leu Leu Cys Gly Ile Leu Phe Ala Phe Ile His
515 520 525

Thr Tyr Arg Asp Ala Asp Asp Leu Ser Lys
530 535

<210> 10
<211> 221
<212> PRT
<213> H. influenzae

<220>
<221> misc_feature
<223> heme exporter protein B (ccmB)

<220>
<221> misc_feature
<223> gi|1574645

<400> 10

Met Ile Phe Leu Glu Ile Ile Lys Arg Glu Leu Gln Ile Ala Met Arg
1 5 10 15

Lys Asn Ala Glu Ile Leu Asn Pro Leu Trp Phe Phe Leu Leu Val Ile
20 25 30

Thr Leu Phe Pro Leu Val Ile Gly Pro Asp Pro Lys Leu Leu Ser Arg
35 40 45

Ile Ala Pro Gly Ile Ala Trp Val Ala Ala Leu Leu Ser Ala Leu Leu
50 55 60

Ser Phe Glu Arg Leu Phe Arg Asp Asp Phe Ile Asp Gly Ser Leu Glu
65 70 75 80

Gln Leu Met Leu Thr Ala Gln Pro Leu Pro Met Thr Ala Leu Ala Lys
85 90 95

Val Val Ala His Trp Leu Leu Thr Gly Leu Pro Leu Ile Leu Leu Ser
100 105 110

Pro Ile Ala Ala Leu Leu Leu Ser Leu Glu Val Asn Ile Trp Trp Ala
 115 120 125

Leu Val Leu Thr Leu Leu Leu Gly Thr Pro Val Leu Ser Cys Ile Gly
 130 135 140

Ala Ile Gly Val Ala Leu Thr Val Gly Leu Arg Lys Gly Gly Val Leu
 145 150 155 160

Leu Ser Leu Leu Val Val Pro Leu Phe Ile Pro Val Leu Ile Phe Ala
 165 170 175

Ser Ser Val Leu Glu Ala Ala Gly Leu Asn Val Pro Tyr Gly Gly Gln
 180 185 190

Leu Ala Ile Leu Gly Ala Met Met Val Gly Ala Val Thr Leu Ser Pro
 195 200 205

Phe Ala Ile Ala Ala Ala Leu Arg Ile Ser Leu Asp Asn
 210 215 220

<210> 11
 <211> 788
 <212> PRT
 <213> H. influenzae

<220>
 <221> misc_feature
 <223> recombination protein (rec2)

<220>
 <221> misc_feature
 <223> gi|1573009

<400> 11

Met Lys Leu Asn Leu Ile Thr Leu Val Val Leu Leu Ile Val Ala Asp
 1 5 10 15

Leu Thr Leu Leu Phe Leu Pro Gln Pro Leu Leu Leu Pro Trp Gln Val
 20 25 30

Ala Leu Val Ile Ala Leu Val Leu Ile Phe Leu Phe Ile Phe Leu Arg
 35 40 45

Arg Asn Phe Leu Val Ser Leu Ala Phe Phe Val Ala Ser Leu Gly Tyr
 50 55 60

Phe His Tyr Ser Ala Leu Ser Leu Ser Gln Gln Ala Gln Asn Ile Thr
65 70 75 80
Ala Gln Lys Gln Val Val Thr Phe Lys Ile Gln Glu Ile Leu His Gln
85 90 95
Gln Asp Tyr Gln Thr Leu Ile Ala Thr Ala Thr Leu Glu Asn Asn Leu
100 105 110
Gln Glu Gln Arg Ile Phe Leu Asn Trp Lys Ala Lys Glu Val Pro Gln
115 120 125
Leu Ser Glu Ile Trp Gln Ala Glu Ile Ser Leu Arg Ser Leu Ser Ala
130 135 140
Arg Leu Asn Phe Gly Gly Phe Asp Arg Gln Gln Trp Tyr Phe Ser Lys
145 150 155 160
Gly Ile Thr Ala Val Gly Thr Val Lys Ser Ala Val Lys Ile Ala Asp
165 170 175
Val Ser Ser Leu Arg Ala Glu Lys Leu Gln Gln Val Lys Lys Gln Thr
180 185 190
Glu Gly Leu Ser Leu Gln Gly Leu Leu Ile Ala Leu Ala Phe Gly Glu
195 200 205
Arg Ala Trp Leu Asp Lys Thr Thr Trp Ser Ile Tyr Gln Gln Thr Asn
210 215 220
Thr Ala His Leu Ile Ala Ile Ser Gly Leu His Ile Gly Leu Ala Met
225 230 235 240
Gly Ile Gly Phe Cys Leu Ala Arg Val Val Gln Val Phe Phe Pro Thr
245 250 255
Arg Phe Ile His Pro Tyr Phe Pro Leu Val Phe Gly Val Leu Phe Ala
260 265 270
Leu Ile Tyr Ala Tyr Leu Ala Gly Phe Ser Val Pro Thr Phe Arg Ala
275 280 285
Ile Ser Ala Leu Val Phe Val Leu Phe Ile Gln Ile Met Arg Arg His
290 295 300

Tyr Ser Pro Ile Gln Phe Phe Thr Leu Val Val Gly Phe Leu Leu Phe
 305 310 315 320

Cys Asp Pro Leu Met Pro Leu Ser Val Ser Phe Trp Leu Ser Cys Gly
 325 330 335

Ala Val Gly Cys Leu Leu Leu Trp Tyr Arg Tyr Val Pro Phe Ser Leu
 340 345 350

Phe Gln Trp Lys Asn Arg Pro Phe Ser Pro Lys Val Arg Trp Ile Phe
 355 360 365

Ser Leu Phe His Leu Gln Phe Gly Leu Leu Leu Phe Phe Thr Pro Leu
 370 375 380

Gln Leu Phe Leu Phe Asn Gly Leu Ser Leu Ser Gly Phe Leu Ala Asn
 385 390 395 400

Phe Met Ala Val Pro Ile Tyr Ser Phe Leu Leu Val Pro Leu Ile Leu
 405 410 415

Phe Ala Val Phe Thr Asn Gly Thr Met Phe Ser Trp Gln Leu Ala Asn
 420 425 430

Lys Leu Ala Glu Gly Ile Thr Gly Leu Ile Ser Val Phe Gln Gly Asn
 435 440 445

Trp Leu Thr Val Ser Phe Asn Leu Ala Leu Gly Leu Thr Ala Leu Cys
 450 455 460

Ala Gly Ile Phe Met Leu Ile Ile Trp Asn Ile Tyr Arg Glu Pro Glu
 465 470 475 480

Ile Ser Ser Ser Asn Trp Gln Ile Lys Arg Ala Lys Phe Phe Thr Leu
 485 490 495

Asn Leu Ser Lys Pro Leu Leu Lys Asn Glu Arg Ile Asn Val Leu Arg
 500 505 510

Cys Ser Phe Gly Ile Ile Leu Leu Cys Phe Thr Ile Leu Leu Phe Lys
 515 520 525

Gln Leu Ser Lys Pro Thr Trp Gln Val Asp Thr Leu Asp Val Gly Gln
 530 535 540

Gly Leu Ala Thr Leu Ile Val Lys Asn Gly Lys Gly Ile Leu Tyr Asp
 545 550 555 560

Thr Gly Ser Ser Trp Arg Gly Gly Ser Met Ala Glu Leu Glu Ile Leu
 565 570 575

Pro Tyr Leu Gln Arg Glu Gly Ile Val Leu Glu Lys Leu Ile Leu Ser
 580 585 590

His Asp Asp Asn Asp His Ala Gly Gly Ala Ser Thr Ile Leu Lys Ala
 595 600 605

Tyr Pro Asn Val Glu Leu Ile Thr Pro Ser Arg Lys Asn Tyr Gly Glu
 610 615 620

Asn Tyr Arg Thr Phe Cys Thr Ala Gly Arg Asp Trp His Trp Gln Gly
 625 630 635 640

Leu His Phe Gln Ile Leu Ser Pro His Asn Val Val Thr Arg Ala Asp
 645 650 655

Asn Ser His Ser Cys Val Ile Leu Val Asp Asp Gly Lys Asn Ser Val
 660 665 670

Leu Leu Thr Gly Asp Ala Glu Ala Lys Asn Glu Gln Ile Phe Ala Arg
 675 680 685

Thr Leu Gly Lys Ile Asp Val Leu Gln Val Gly His His Gly Ser Lys
 690 695 700

Thr Ser Thr Ser Glu Tyr Leu Leu Ser Gln Val Arg Pro Asp Val Ala
 705 710 715 720

Ile Ile Ser Ser Gly Arg Trp Asn Pro Trp Lys Phe Pro His Tyr Ser
 725 730 735

Val Met Glu Arg Leu His Arg Tyr Lys Ser Ala Val Glu Asn Thr Ala
 740 745 750

Val Ser Gly Gln Val Arg Val Asn Phe Phe Gln Asp Arg Leu Glu Ile
 755 760 765

Gln Gln Ala Arg Thr Lys Phe Ser Pro Trp Tyr Ala Arg Val Ile Gly
 770 775 780

Leu Ser Lys Glu
785

<210> 12
<211> 505
<212> PRT
<213> H. pylori

<220>
<221> misc_feature
<223> poly E-rich protein

<220>
<221> misc_feature
<223> gi|2313421

<400> 12

Met Lys Met Ile Leu Phe Asn Gln Asn Pro Met Ile Thr Lys Leu Leu
1 5 10 15

Glu Ser Val Ser Lys Lys Leu Glu Leu Pro Ile Glu Asn Phe Asn His
20 25 30

Tyr Gln Glu Leu Ser Ala Arg Leu Lys Glu Asn Gln Glu Trp Leu Leu
35 40 45

Ile Ala Asp Asp Glu Cys Leu Glu Lys Leu Asp Gln Val Asp Trp Leu
50 55 60

Glu Leu Lys Glu Thr Ile Ser Gln Asn Lys Asn Ser Val Cys Met Tyr
65 70 75 80

Lys Lys Gly Asn Glu Ala Gln Pro Phe Leu Glu Gly Phe Glu Val Lys
85 90 95

Ile Lys Lys Pro Phe Leu Pro Thr Glu Met Leu Lys Val Leu Gln Lys
100 105 110

Lys Leu Gly Ser Asn Ala Ser Glu Leu Glu Pro Ser Gln Asn Leu Asp
115 120 125

Pro Thr Gln Glu Val Leu Glu Thr Asn Trp Asp Glu Leu Glu Asn Leu
130 135 140

Gly Asp Leu Glu Ala Leu Val Gln Glu Glu Pro Asn Asn Glu Glu Gln
145 150 155 160

Leu Leu Pro Thr Leu Asn Asp Gln Glu Glu Lys Glu Glu Val Lys Glu
 165 170 175

Glu Glu Lys Glu Glu Val Lys Glu Glu Glu Lys Glu Glu Val Lys Glu
 180 185 190

Glu Glu Lys Glu Glu Val Lys Glu Thr Pro Gln Glu Glu Lys Lys Pro
 195 200 205

Lys Asp Asp Glu Thr Gln Glu Gly Glu Thr Leu Lys Asp Lys Glu Val
 210 215 220

Ser Lys Glu Leu Glu Ala Pro Gln Glu Leu Glu Ile Pro Lys Glu Glu
 225 230 235 240

Thr Gln Glu Gln Asp Pro Ile Lys Glu Glu Thr Gln Glu Asn Lys Glu
 245 250 255

Glu Lys Gln Glu Lys Thr Gln Asp Ser Pro Ser Ala Gln Glu Leu Glu
 260 265 270

Ala Met Gln Glu Leu Val Lys Glu Ile Gln Glu Asn Ser Asn Gly Gln
 275 280 285

Glu Asn Lys Glu Lys Thr Gln Glu Ser Ala Glu Ile Pro Gln Asp Lys
 290 295 300

Glu Ile Gln Glu Val Val Thr Glu Lys Thr Gln Ala Gln Glu Leu Glu
 305 310 315 320

Val Pro Lys Glu Lys Thr Gln Glu Ser Ala Glu Ala Leu Gln Glu Thr
 325 330 335

Gln Ala His Glu Leu Glu Lys Gln Glu Ile Ala Glu Thr Pro Gln Asp
 340 345 350

Val Glu Ile Pro Gln Ser Gln Asp Lys Glu Val Gln Glu Leu Glu Ile
 355 360 365

Pro Lys Glu Glu Thr Gln Glu Asn Thr Glu Thr Pro Gln Asp Val Glu
 370 375 380

Thr Pro Gln Glu Lys Glu Thr Gln Glu Asp His Tyr Glu Ser Ile Glu
 385 390 395 400

Asp Ile Pro Glu Pro Val Met Ala Lys Ala Met Gly Glu Glu Leu Pro
405 410 415

Phe Leu Asn Glu Ala Val Ala Lys Ile Pro Asn Asn Glu Asn Asp Thr
420 425 430

Glu Thr Pro Lys Glu Ser Val Thr Glu Thr Ser Lys Asn Glu Asn Asn
435 440 445

Thr Glu Thr Pro Gln Glu Lys Glu Glu Ser Asp Lys Thr Ser Ser Pro
450 455 460

Leu Glu Leu Arg Leu Asn Leu Gln Asp Leu Leu Lys Ser Leu Asn Gln
465 470 475 480

Glu Ser Leu Lys Ser Leu Leu Glu Asn Lys Thr Leu Ser Ile Lys Ile
485 490 495

Thr Leu Glu Asp Lys Lys Pro Asn Ala
500 505

<210> 13
<211> 60
<212> PRT
<213> H. pylori

<220>
<221> misc_feature
<223> histidine-rich, metal binding polypeptide (hpn)

<220>
<221> misc_feature
<223> gi|2314604

<400> 13

Met Ala His His Glu Glu Gln His Gly Gly His His His His His His
1 5 10 15

His Thr His His His His Tyr His Gly Gly Glu His His His His His
20 25 30

His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
35 40 45

His Gln Glu Glu Gly Cys Cys His Gly His His Glu
50 55 60

<210> 14
<211> 72
<212> PRT
<213> H. pylori

<220>
<221> misc_feature
<223> histidine and glutamine-rich protein

<220>
<221> misc_feature
<223> gi|2314605

<400> 14

Met Ala His His Glu Gln Gln Gln Gln Gln Gln Ala Asn Ser Gln His
1 5 10 15

His His His His His Ala His His His His Tyr Tyr Gly Gly Glu His
20 25 30

His His His Asn Ala Gln Gln His Ala Glu Gln Gln Ala Glu Gln Gln
35 40 45

Ala Gln Gln Gln Gln Gln Gln Gln Ala His Gln Gln Gln Gln Lys
50 55 60

Ala Gln Gln Gln Asn Gln Gln Tyr
65 70

<210> 15
<211> 1139
<212> PRT
<213> M. genitalium

<220>
<221> misc_feature
<223> cytoadherence-accessory protein

<220>
<221> misc_feature
<223> gi|1046012

<400> 15

Met Ala Lys Asn Lys Gln Ser Val Phe Glu Glu Lys Asn Tyr Thr Gln
1 5 10 15

Thr Glu Pro Glu Asn Ile Phe Gly Asp Leu Tyr Asp Gly Lys Ser Thr
20 25 30

Val Glu Glu Asp Pro Asn Ile Lys Val Ala Tyr Asp Ala Asp Gly Asn
 35 40 45

Gly Tyr Tyr Ile Ala Phe Asn Lys Glu Thr Gly Val Tyr Tyr Asp Pro
 50 55 60

Tyr Gly Asp Thr Glu Tyr Asp Ile Ser Gln Leu Phe Asp Glu Asn Gly
 65 70 75 80

Asn Pro Phe Val Phe Asp Glu Lys Gln Glu Glu Asn Asp Tyr Leu Lys
 85 90 95

Tyr Val Gly Asn Pro Asp Tyr Gly Ser Tyr Asp Glu Asn Gly Glu Trp
 100 105 110

Val Trp Ser Gly Tyr Phe Glu Asn Asp Gln Trp Ile Ser Thr Lys Glu
 115 120 125

Ser Gln Pro Thr Asp Glu Asn Tyr Gly Phe Asp Ser Asp Leu Pro Pro
 130 135 140

Glu Val Lys Gln Pro Glu Ser Val Glu Asp Asn Tyr Gly Phe Asp Asn
 145 150 155 160

Asp Leu Pro Pro Glu Val Lys Gln Pro Glu Ser Val Glu Asp Asn Tyr
 165 170 175

Gly Phe Asp Asn Asp Leu Pro Pro Glu Val Lys Gln Pro Glu Ser Val
 180 185 190

Val Asp Gln Pro Ser Ser Asp Asp Tyr Phe Ala Lys Gln Pro Thr Asp
 195 200 205

Glu Asn Tyr Gly Phe Asp Asn Asp Leu Pro Pro Glu Val Lys Gln Pro
 210 215 220

Glu Ser Val Val Asp Gln Pro Ser Ser Asp Asp His Phe Ala Lys Gln
 225 230 235 240

Pro Glu Ser Thr Thr Asp Ser Tyr Ser Phe Asp Ser Asp Leu Pro Gln
 245 250 255

Pro Thr Leu Asp Gln Pro Ser Leu Asp Asp His Val Gln Tyr Asn Phe
 260 265 270

Asp His His Glu Glu Leu Lys Pro Val Ala Glu Glu Gln Asn Asn Tyr
275 280 285

Gln Val Gly Phe Asp Gln Val Gln Ala Asn Leu Asp Asn Asn Glu Glu
290 295 300

Ile Gln Pro Thr Ala Glu Lys Lys Val Thr Thr Asp Phe Glu Ser Lys
305 310 315 320

Gln Ala Gln Val Val Asp Ser Tyr Gln Leu Pro Ile Asp Thr Asp Gln
325 330 335

Gln Asp Gln Thr Thr Phe Ser Ser Ser Phe Glu Thr Gln Pro Thr Val
340 345 350

Glu Gln Phe Asp Gln Val Asn Ser Glu Val Asn Asp Gln Phe Lys Pro
355 360 365

Glu Ile Thr Lys Glu Pro Val Leu Glu Ser Ser Phe Asn Lys Gln Asp
370 375 380

Val Val Glu Thr Ser Asp Leu Asn Ser Glu Ser Asn Leu Tyr Ser Glu
385 390 395 400

Asn Asn Lys Asp Ala Thr Asn Asn Asp Ser Leu Asn Ser Glu Phe Ile
405 410 415

Gln Leu Asn Ser Asn Ser Glu Thr Ala Ser Asp Asp Val His Tyr Glu
420 425 430

Ser Lys Ser Glu Pro Ile His Asp Tyr Lys Phe Gly Ser Asp Leu Ser
435 440 445

Gln Ser Asn Ser Asn Asn Ser Leu Glu Ser Glu Pro Val Lys Phe Asn
450 455 460

Ser Glu Thr Ala Pro Asp Ala His Phe Glu Ser Gln Ser Glu Pro Val
465 470 475 480

Asp Gln Val Gln Tyr Asp Ile Tyr Gln Asn Glu Glu Leu Lys Pro Thr
485 490 495

Leu Asp Gln Pro Ser Ser Asp Asp Tyr Phe Ala Lys Gln Pro Thr Asp
500 505 510

Glu Asn Tyr Gly Phe Asp Asn Asp Leu Pro Pro Glu Val Lys Gln Pro
515 520 525

Glu Ser Val Val Asp Gln Pro Ser Ser Asp Asp His Phe Ala Lys Gln
530 535 540

Pro Glu Ser Thr Thr Asp Ser Tyr Ser Phe Asp Ser Asp Leu Pro Gln
545 550 555 560

Pro Thr Leu Asp Gln Pro Ser Leu Asp Asp His Val Gln Tyr Asn Phe
565 570 575

Asp His His Glu Glu Leu Lys Pro Val Ala Glu Glu Gln Asn Asn Tyr
580 585 590

Gln Val Gly Phe Asp Gln Val Gln Ala Asn Leu Asp Asn Asn Glu Glu
595 600 605

Ile Gln Pro Thr Ala Glu Lys Glu Val Thr Thr Asp Phe Glu Ser Lys
610 615 620

Gln Ala Gln Val Val Asp Ser Tyr Gln Leu Pro Ile Asp Thr Asp Gln
625 630 635 640

Gln Asp Gln Thr Thr Phe Ser Ser Ser Phe Glu Thr Gln Pro Thr Val
645 650 655

Glu Gln Phe Asp Gln Val Asn Ser Glu Val Asn Asp Gln Phe Lys Pro
660 665 670

Glu Ile Thr Lys Glu Pro Val Leu Glu Ser Ser Phe Asn Lys Gln Asp
675 680 685

Val Val Glu Thr Ser Asn Tyr Thr Asn Asn Leu Gln Lys Phe Asp Ile
690 695 700

Gln Ser Asp Asn Lys Ile Thr Ile Thr Thr Lys Lys Ser Ser Pro Gln
705 710 715 720

Ile Pro Thr Thr Leu Pro Ile Ser Phe Val Ser Asn Arg Ile Glu Tyr
725 730 735

Lys Pro Val Glu Thr Leu Ala Leu Asp Asn Lys Glu Ser Gln Gln Glu
740 745 750

Gln Ile Thr Ile Asn Ser Ile Thr Glu Asp Ser Lys Thr Leu Ala Lys
755 760 765

Thr Leu Ser Val Gln Leu Gln Gln Ile Asn Ser Leu Asn Asn Gln Ser
770 775 780

Ile Val Thr Ser Glu Ser Val Arg Leu Asp Lys Lys Asp Asp Gln Leu
785 790 795 800

Thr Ile Asn Thr Val Asn Ser Glu Asp Gln Gln Pro Lys Ile Glu Val
805 810 815

Phe Val Lys Ala Lys Glu Pro Val Glu Glu His Ser Ile Thr Gln Asn
820 825 830

Lys Gln Ser Val Glu Asp Lys Ser Glu Leu Asp Asn Phe Asn Lys Lys
835 840 845

Ser Asp Leu Tyr Lys Ile Ile Ser Glu Leu Lys Arg Gly Glu Leu Asn
850 855 860

Pro Thr Ile Asn Phe Asp Ala Ile Phe Gln Met Asn Asp Tyr Gln Met
865 870 875 880

Ser Val Lys Gln Ser Phe Ile His Leu Asn Asp Phe Val Thr Asn Tyr
885 890 895

Lys Asn Gln Ile Ser Glu Arg Tyr Leu Ile Ile Lys Lys Glu Leu Gln
900 905 910

Ser Glu Leu Ser Arg Leu Ile Asp Gln Asn Glu Asn Leu Asn Val Gln
915 920 925

Phe Asn Asn Ala Lys Asn Leu Thr Thr Leu Gln Lys Glu Glu Met Ile
930 935 940

Arg Ser Leu Ala Ser Asp Phe Ala Ile Ala Tyr Lys Pro Ser Asn Ser
945 950 955 960

Tyr Glu Gln Leu Gln Lys Ser Gly Glu Ile Met Arg His Val Gln Arg
965 970 975

Ala Ile Thr Glu Asn Glu Lys Lys Ile Glu Ser Ile Gln Gly Ser Leu
980 985 990

Lys Gln Leu Lys Thr Val Tyr Asn Ser Cys Cys Glu Thr Ile Met Asn
 995 1000 1005

Asn Ile Asn Lys Leu Asp Asn Thr Leu Arg Phe Ala Lys Lys Glu
 1010 1015 1020

Lys Asp Pro Leu Leu Leu Ser Asn Phe Asp Ser Val Thr Asp Asn
 1025 1030 1035

Gly Leu Val Glu Pro Asn Gln Leu Met Asp Asp Leu Ile Asp Phe
 1040 1045 1050

Ser Asn Thr Phe Asp Asn Ile Ser Asn Glu Gln Leu Asp Asp Phe
 1055 1060 1065

Ile Tyr Glu Asn Met Asp Arg Asn Ile Asp Phe Glu Phe Glu Gly
 1070 1075 1080

Phe Asn Asn Asp Phe Val Asp Ile Asp Ala Lys Val Met Asp Ser
 1085 1090 1095

Met Ser Ala Phe Ser Val Asn Asp Leu Asp Ile Glu Thr Leu Val
 1100 1105 1110

Pro Asp Arg Thr Ser Asn Phe Ser Ser Leu Leu Asp Glu Asp Leu
 1115 1120 1125

Phe Glu Ser Ser Gly Asp Phe Ser Leu Asp Tyr
 1130 1135

<210> 16
 <211> 1616
 <212> PRT
 <213> M. genitalium

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 <223> cytaadherence-accessory protein

<220>
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 <223> gi|1046097

<400> 16

Met Pro Lys Thr Thr Lys Asn Lys Asn Lys Asn Thr Thr Pro Lys Ser
 1 5 10 15

Lys Thr Lys Lys Tyr Leu Glu Ser Ala Asn Lys Lys Ser Val Thr Lys
 20 25 30

Pro Lys Lys Glu Gln Asp Lys Val Glu Asn Leu Phe Asp Gln Pro Phe
 35 40 45

Leu Gly Glu Ile Lys Lys Asn Ile Leu Lys Lys Thr Lys Ser Phe Asn
 50 55 60

Ser Lys Lys Lys Glu Thr Val Lys Ser Lys Ser Lys Ser Pro Ile Asp
 65 70 75 80

Phe Phe Asp Glu Thr Lys Arg Gly Val Phe Ile Val Pro Pro Glu Thr
 85 90 95

Asp Ile Leu Ser Arg Arg Glu Leu Asn Gln Lys Thr Val Val Asn Thr
 100 105 110

Val Pro Asn Gln Thr Ser Ser Tyr Pro Thr Ile Asn Glu Asn Lys Leu
 115 120 125

Val Glu Leu Asn Asn Gln Pro Glu Thr Lys Val Leu Glu Thr Lys Lys
 130 135 140

Asp Ser Phe Thr Thr Thr Ile Arg Glu Lys Lys Leu Asn Pro Glu Asp
 145 150 155 160

Ser Gln Ala Phe Trp Tyr Ile Phe Val Gly Asp Arg Lys Tyr Gly Phe
 165 170 175

Trp Lys Asn His Thr Trp Val Trp Leu Gly Tyr Phe Asp Gln Leu Gln
 180 185 190

Arg Trp Asn Tyr Phe Lys Val Ile Glu Thr Val Glu Val Pro Gln Glu
 195 200 205

His Ala Ala Phe Ile Lys Gln Arg Pro Ala Asp Ile Asp Phe Trp Arg
 210 215 220

Pro Leu Val Gly Asn Pro Asn Tyr Gly Phe Val Gln Asn Asn Thr Trp
 225 230 235 240

Ile Trp Lys Gly Phe Phe Asp Lys Lys Leu Asn Trp Ile Pro Asp Pro
 245 250 255

Val Arg Phe Thr Glu Glu Ala Leu Gly His Thr Asp Ser Leu Val Asp
260 265 270

Glu Ile Glu Lys Lys Thr Ile Ser Glu Gln Pro Tyr Trp Glu Gln Glu
275 280 285

Asn Asp Ile Val Val Thr Val Phe Asn Thr Lys Ser Leu Ala Ser Ser
290 295 300

Leu Glu Asn Glu Leu Leu Leu Glu Asn Ser Ser Glu Glu Gln Pro Val
305 310 315 320

Ile Glu Glu Val Lys Pro Arg Arg Asn Glu Val Ile Phe Arg Asn Pro
325 330 335

Val Thr Lys Leu His Phe Glu Lys Glu Lys Phe Glu Phe Leu Asn Pro
340 345 350

Val Lys Glu Thr Asn Glu Thr Ile Pro Leu Ile Glu Ile Val Lys Glu
355 360 365

Glu Val Lys Val Glu Ser Glu Val Glu Ala Pro Val Glu Ile Glu Pro
370 375 380

Glu Ala Ala Cys Glu Pro Glu Thr Thr Ile Pro Glu Val Glu Thr Val
385 390 395 400

Phe Val Tyr Glu Asp Asp Leu Lys Gly Leu Asp Ser Asn Gln Thr Gln
405 410 415

Ala Gly Asn Val Pro Glu Val Glu Thr Val Phe Val Tyr Glu Asp Asp
420 425 430

Leu Lys Gly Leu Asp Ser Ile Ile Lys Asp Asp Gln Gln His Asp Glu
435 440 445

Ile Ala Lys His Val Glu His Leu Ser Gln Asp Tyr Ser Lys Glu Ile
450 455 460

Lys Asp Ser Ala Lys Ala Asp Leu Ser Asn Ile Ser Asp Asp Ile Asp
465 470 475 480

Ser Val Trp Lys Glu Phe Gly Ser Phe Thr Asp Glu Thr Gln Lys Ser
485 490 495

Val Glu Glu Lys Ser Gln Val Asp Glu Ile Ile Leu Asp Ala Asn Asn
500 505 510

Asp Phe Ile Asn Glu Ser Leu Phe Arg Asp Glu Val Val Asn Asn Ile
515 520 525

Asp Ser Gln Ile Asn Glu Thr Val Ser Glu Gln Gln Phe Glu Pro Thr
530 535 540

Tyr Ser Val Asn Glu Phe Gln Gln Glu Phe Ser Glu Pro Val Val Ser
545 550 555 560

Asp Glu Lys Ile Lys Glu Thr Asn Ser Asp Glu Ser Val Asn Thr Asp
565 570 575

Leu Thr Ala Leu Phe Ser Glu Lys Leu Val Asn Glu Val Leu Leu Thr
580 585 590

Asn Glu Tyr Val Asp Val Asn Ala Pro Phe Ser Thr Glu Thr Glu Val
595 600 605

Lys Val Ser Ser Glu Leu Pro Lys Ser Glu Leu Val Asp Glu Ile Thr
610 615 620

Phe Ile Asn Asn Asp Pro Lys Pro Gln Glu Gly Leu Glu Tyr Lys Val
625 630 635 640

Asp Phe Leu Glu Thr Glu Pro Lys Ser Leu Phe Asp Glu Lys Thr Thr
645 650 655

Ile Val Val Glu Ser Glu Pro Pro Phe Ile Gln Pro Asp Leu Ser Leu
660 665 670

Glu Leu Asp Ser Val Asn Asp Val Asp Lys Ser Leu Glu Thr Lys Thr
675 680 685

Thr Ser Val Glu Leu Asn His Glu Glu Ile Gly Asn Glu Phe Ile Asn
690 695 700

Leu Asp Val Ser Glu Lys Glu Val Gln Glu Gln Pro Thr Thr Gln Leu
705 710 715 720

Glu Thr Asp Ser Glu Phe Val Leu Pro Thr Tyr Gln Ile Val Glu Asp
725 730 735

Ser Phe Thr Glu Ser Ala Glu Thr Pro Asn Glu Phe Ser Ser Glu Gln
740 745 750

Lys Asp Thr Leu Glu Phe Ile Ser Gln Thr Gln Glu Val Glu Thr Ser
755 760 765

Glu Ser Asn Val Pro Thr Val Glu Gln Glu Thr Lys Leu Phe Glu His
770 775 780

Gln Asp Glu Asn Asn Leu Phe Thr Pro Leu Pro Leu Asp Leu Thr Glu
785 790 795 800

Ile Ile Glu Ser Asn Ala Leu Phe Asp Ser Lys Pro Asp Glu Lys Glu
805 810 815

Ser Ser Asp Ser Glu Leu Gln Pro Thr Phe Lys Glu Ile Lys Leu Asp
820 825 830

Ser Thr Val Glu Val Pro Gln Glu Ser Ser Gln Val Glu Ala Thr Phe
835 840 845

Asp Thr Val Gln Pro Glu Ala Val Phe Asp Glu Ile Lys Thr Gln Glu
850 855 860

Leu Gln Pro Glu Ala Thr Thr Glu Val Val Phe Asp Asp His Phe Gln
865 870 875 880

Pro Asp Val Gln Pro Glu Gln Thr Pro Gln Glu Ala Lys Phe Asp Ser
885 890 895

Pro Val Glu Ile Pro Gln Glu Ser Ser Gln Ala Glu Phe His Ala Glu
900 905 910

Gln Ile Ser Asp Glu Ile Lys Leu Glu Glu Lys Thr Glu Ala Val Phe
915 920 925

Asp His Gln Gln Leu Glu Asn Gln Ser Glu Glu Thr Val Val Thr Pro
930 935 940

Thr Glu Val Thr Ala Phe Glu Pro Glu Thr Ile Glu Thr Gln Leu Glu
945 950 955 960

Pro Ser Ser Glu Asp Gln Pro Ser Glu Pro Ala Leu Asp Gln Asn His
965 970 975

Pro Glu Ile Val Thr Ala Glu Val Glu Gln Ile Phe Asp Gly Thr Lys
980 985 990

Leu Glu Asp Leu Lys Leu Glu Glu Ala Asn Phe Asp Asn Val Glu Asn
995 1000 1005

Asn Glu Val Gln Pro Lys Glu Thr Glu Ala Glu Ile Thr Phe Asp
1010 1015 1020

Glu Thr Lys Glu Leu Gln Gln Glu Thr Ser Ser Glu Pro Leu Ser
1025 1030 1035

Thr Glu Glu Leu Lys Ser Glu Ala Thr Phe Asp Asn Val Ser Glu
1040 1045 1050

Ala Glu Ser Glu Ala Val Phe Glu Lys Pro Gln Leu Glu Thr Gln
1055 1060 1065

Thr Glu Lys Ile Leu Glu Glu Glu Pro Lys Ser Glu Pro Val Asp
1070 1075 1080

Gln Leu Ile Thr Glu Ala Ser Phe Asp Thr Val Lys His Glu Ala
1085 1090 1095

Val Phe Asp Lys Asn Gln Thr Gln Thr Glu Gly Leu Glu Glu Pro
1100 1105 1110

Gln Val Ser Ser Glu Ala Glu Val Val Asp Gln Thr Thr Thr Asp
1115 1120 1125

Thr Val Gly Glu Pro Glu Ala Val Phe Asp Val Gln Pro Glu Lys
1130 1135 1140

Thr Thr Glu Val Lys Phe Asp Asp Val Glu Asn Gln Gln Lys Val
1145 1150 1155

Ile Ser Glu Pro Gln Val Glu Gln Gln Pro Gly Glu Ala Val Phe
1160 1165 1170

Glu Pro Ser Ala Glu Ala Lys Phe Asp Ser Pro Val Glu Ser Val
1175 1180 1185

Gln Asp Ser Gln Pro Glu Pro Val Leu Glu Glu Val Gln Thr Gln
1190 1195 1200

Pro	Glu	Ile	Gln	Pro	Val	Glu	Ser	Gln	Pro	Glu	Ala	Thr	Phe	Asp
1205						1210					1215			
Thr	Val	Gln	Pro	Glu	Gln	Thr	Pro	Gln	Glu	Ala	Lys	Phe	Asp	Ser
1220						1225					1230			
Pro	Val	Glu	Thr	Val	Glu	Gln	Pro	Glu	Phe	Ser	Ser	Glu	Pro	Thr
1235						1240					1245			
Gln	Gln	His	Val	Glu	Ser	Glu	Ala	Ser	Phe	Asp	Glu	Pro	Asn	Tyr
1250						1255					1260			
Asp	Phe	Asp	Glu	Pro	Asn	Tyr	Asp	Phe	Asp	Gln	Pro	Ser	Tyr	Asp
1265						1270					1275			
Ser	Asp	Leu	Gln	Pro	Ser	Glu	Pro	Gln	Tyr	Asp	Val	Asp	Glu	Pro
1280						1285					1290			
Asn	Tyr	Asp	Phe	Asp	Glu	Pro	Asn	Tyr	Glu	Ile	Glu	Ser	Lys	Pro
1295						1300					1305			
Ser	Glu	Pro	Gln	Phe	Glu	Pro	Gln	Val	Glu	Gln	Gln	Pro	Gly	Glu
1310						1315					1320			
Ala	Val	Phe	Glu	Pro	Ser	Ala	Glu	Ala	Lys	Phe	Asp	Ser	Pro	Val
1325						1330					1335			
Glu	Ser	Val	Gln	Asp	Ser	Gln	Pro	Glu	Pro	Leu	Leu	Glu	Glu	Val
1340						1345					1350			
Gln	Thr	Gln	Pro	Glu	Ile	Gln	Pro	Val	Glu	Ser	Gln	Pro	Glu	Ala
1355						1360					1365			
Thr	Phe	Asp	Thr	Val	Gln	Pro	Glu	Gln	Thr	Pro	Gln	Glu	Ala	Lys
1370						1375					1380			
Phe	Asp	Ser	Pro	Val	Glu	Thr	Ile	Gln	Glu	Pro	Gln	Val	Ser	Ser
1385						1390					1395			
Glu	Pro	Glu	Val	Val	Val	Gln	Pro	Asn	Phe	Glu	Glu	Arg	Lys	Pro
1400						1405					1410			
Glu	Thr	Val	Leu	Glu	Glu	Pro	Gln	Ala	Asp	Glu	Ile	Gln	Pro	Glu
1415						1420					1425			

Ala Ser Glu Glu Glu Ser Leu Asp Trp Glu Leu Leu Val Gly Asn
1430 1435 1440

Asn Ser Tyr Gly His Tyr Glu Pro Asp Gly Glu Trp Val Trp Ala
1445 1450 1455

Gly Phe Phe Gly Asp Asp Gln Lys Trp Asn Lys Asp Ala Thr Val
1460 1465 1470

Lys Trp Ala Arg Glu Arg Asp Tyr Leu Pro Leu Ile Gly Asp Glu
1475 1480 1485

Val Tyr Gly Arg Tyr Asn Asn Lys Gly Glu Trp Ile Trp Tyr Gly
1490 1495 1500

Phe Tyr Asp Glu Ser Gly Asp Trp Val Leu Val Asp Glu Gln Trp
1505 1510 1515

Lys Asn Arg Gln Pro Arg Ile Asn Glu Ala Pro Lys Phe Trp Glu
1520 1525 1530

Lys Leu Ile Gly Asn Glu Glu Tyr Gly Tyr Tyr Glu Asp Asn Glu
1535 1540 1545

Trp Asn Trp Tyr Asp Gly Glu Phe Asp Ser Glu Gly Asn Trp Leu
1550 1555 1560

Val Phe Gln Ser Glu Glu Thr Glu Asn Leu Asn Glu Asp Ile Thr
1565 1570 1575

Lys Asp Ile Pro Ala Leu Glu Gly Tyr Asp Ile Asp Ser Ile Asp
1580 1585 1590

Ala Asp Glu Trp Leu Ser Gln Phe Ser Ala Asp Asp Ala Lys Asp
1595 1600 1605

Val Phe Gly Ser Asn Asp Lys Lys
1610 1615

<210> 17
<211> 274
<212> PRT
<213> M. pneumoniae

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<221> misc_feature
<223> 30K adhesin-related protein

<220>
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<223> gi|1674069

<400> 17

Met Lys Leu Pro Pro Arg Arg Lys Leu Lys Leu Phe Leu Leu Ala Trp
1 5 10 15

Met Leu Val Leu Phe Ser Ala Leu Ile Val Leu Ala Thr Leu Ile Leu
20 25 30

Val Gln His Asn Asn Thr Glu Leu Thr Glu Val Lys Ser Glu Leu Ser
35 40 45

Pro Leu Asn Val Val Leu His Ala Glu Glu Asp Thr Val Gln Ile Gln
50 55 60

Gly Lys Pro Ile Thr Glu Gln Ala Trp Phe Ile Pro Thr Val Ala Gly
65 70 75 80

Cys Phe Gly Phe Ser Ala Leu Ala Ile Ile Leu Gly Leu Ala Ile Gly
85 90 95

Leu Pro Ile Val Lys Arg Lys Glu Lys Arg Leu Leu Glu Glu Lys Glu
100 105 110

Arg Gln Glu Gln Leu Ala Glu Gln Leu Gln Arg Ile Ser Ala Gln Gln
115 120 125

Glu Glu Gln Gln Ala Leu Glu Gln Gln Ala Ala Glu Ala His Ala
130 135 140

Glu Ala Glu Val Glu Pro Ala Pro Gln Pro Val Pro Val Pro Pro Gln
145 150 155 160

Pro Gln Val Gln Ile Asn Phe Gly Pro Arg Thr Gly Phe Pro Pro Gln
165 170 175

Pro Gly Met Ala Pro Arg Pro Gly Met Pro Pro His Pro Gly Met Ala
180 185 190

Pro Arg Pro Gly Phe Pro Pro Gln Pro Gly Met Ala Pro Arg Pro Gly
195 200 205

Met Pro Pro His Pro Gly Met Ala Pro Arg Pro Gly Phe Pro Pro Gln
210 215 220

Pro Gly Met Ala Pro Arg Pro Gly Met Pro Pro His Pro Gly Met Ala
225 230 235 240

Pro Arg Pro Gly Phe Pro Pro Gln Pro Gly Met Ala Pro Arg Pro Gly
245 250 255

Met Gln Pro Pro Arg Pro Gly Met Pro Pro Gln Pro Gly Phe Pro Pro
260 265 270

Lys Arg

<210> 18
<211> 256
<212> PRT
<213> M. tuberculosis

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<221> misc_feature
<223> PE_PGRS

<220>
<221> misc_feature
<223> gi|3261822

<400> 18

Met Ile Gly Asp Gly Ala Asn Gly Gly Pro Gly Gln Pro Gly Gly Pro
1 5 10 15

Gly Gly Leu Leu Tyr Gly Asn Gly Gly His Gly Gly Ala Gly Ala Ala
20 25 30

Gly Gln Asp Arg Gly Ala Gly Asn Ser Ala Gly Leu Ile Gly Asn Gly
35 40 45

Gly Ala Gly Gly Ala Gly Gly Asn Gly Gly Ile Gly Gly Ala Gly Ala
50 55 60

Pro Gly Gly Leu Gly Gly Asp Gly Gly Lys Gly Gly Phe Ala Asp Glu
65 70 75 80

Phe Thr Gly Gly Phe Ala Gln Gly Gly Arg Gly Gly Phe Gly Gly Asn
85 90 95

Gly Asn Thr Gly Ala Ser Gly Gly Met Gly Gly Ala Gly Gly Ala Gly
100 105 110

Gly Ala Gly Gly Ala Gly Gly Leu Leu Ile Gly Asp Gly Gly Ala Gly
115 120 125

Gly Ala Gly Gly Ile Gly Gly Ala Gly Gly Val Gly Gly Gly Gly Gly
130 135 140

Ala Gly Gly Thr Gly Gly Gly Gly Val Ala Ser Ala Phe Gly Gly Gly
145 150 155 160

Asn Ala Phe Gly Gly Arg Gly Gly Asp Gly Gly Asp Gly Gly Asp Gly
165 170 175

Gly Thr Gly Gly Ala Gly Gly Ala Arg Gly Ala Gly Gly Ala Gly Gly
180 185 190

Ala Gly Gly Trp Leu Ser Gly His Ser Gly Ala His Gly Ala Met Gly
195 200 205

Ser Gly Gly Glu Gly Gly Ala Gly Gly Gly Gly Gly Ala Arg Gly Glu
210 215 220

Ala Gly Ala Gly Gly Gly Thr Ser Thr Gly Thr Asn Pro Gly Lys Ala
225 230 235 240

Gly Ala Pro Gly Thr Gln Gly Asp Ser Gly Asp Pro Gly Pro Pro Gly
245 250 255

<210> 19
<211> 484
<212> PRT
<213> M. tuberculosis

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<221> misc_feature
<223> PE_PGRS

<220>
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<223> gi|2894254

<400> 19

Ala Gln Ala Ser Pro Ala Ala His Gly Gly Ser Gly Gly Ala Gly Gly
1 5 10 15

Asn Gly Gly Ala Gly Ser Ala Gly Asn Gly Gly Ala Gly Gly Ala Gly
 20 25 30

Gly Asn Gly Gly Ala Gly Gly Asn Gly Gly Gly Gly Asp Ala Gly Asn
 35 40 45

Ala Gly Ser Gly Gly Asn Gly Gly Lys Gly Gly Asp Gly Val Gly Pro
 50 55 60

Gly Ser Thr Gly Gly Ala Gly Gly Lys Gly Gly Ala Gly Ala Asn Gly
 65 70 75 80

Gly Ser Ser Asn Gly Asn Ala Arg Gly Gly Asn Ala Gly Asn Gly Gly
 85 90 95

His Gly Gly Ala Gly Gly Ser Gly Asp Thr Gly Gly Ala Gly Gly Ala
 100 105 110

Gly Gly Gln Gly Gly Phe Gly Gly Thr Gly Gly Ser Gly Ser Gly Ile
 115 120 125

Gly Gly Gly Ala Gly Gly Asn Gly Gly Asn Gly Gly Ala Gly Gly Thr
 130 135 140

Gly Val Val Leu Gly Gly Lys Gly Gly Asp Gly Gly Asn Gly Asp His
 145 150 155 160

Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly Ala Gly
 165 170 175

Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly Ser Gly
 180 185 190

Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe Gly Ala
 195 200 205

Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly Gly Asn
 210 215 220

Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser Gly Gly
 225 230 235 240

Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly Gly Ser
 245 250 255

Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala Gly Gly
260 265 270

Ala Gly Gly Ala Gly Gly Asn Gly Ser Leu Ser Ser Gly Glu Gly Gly
275 280 285

Lys Gly Gly Asp Gly Gly His Gly Gly Asp Gly Val Gly Gly Asn Ser
290 295 300

Ser Val Thr Gln Gly Gly Ser Gly Gly Gly Gly Gly Ala Gly Gly Ala
305 310 315 320

Gly Gly Ser Gly Phe Phe Gly Gly Lys Gly Gly Phe Gly Gly Asp Gly
325 330 335

Gly Gln Gly Gly Pro Asn Gly Gly Gly Thr Val Gly Thr Val Ala Gly
340 345 350

Gly Gly Gly Asn Gly Gly Val Gly Gly Arg Gly Gly Asp Gly Val Phe
355 360 365

Ala Gly Ala Gly Gly Gln Gly Gly Leu Gly Gly Gln Gly Gly Asn Gly
370 375 380

Gly Gly Ser Thr Gly Gly Asn Gly Gly Leu Gly Gly Ala Gly Gly Gly
385 390 395 400

Gly Gly Asn Ala Pro Asp Gly Gly Phe Gly Gly Asn Gly Gly Lys Gly
405 410 415

Gly Gln Gly Gly Ile Gly Gly Gly Thr Gln Ser Ala Thr Gly Leu Gly
420 425 430

Gly Asp Gly Gly Asp Gly Gly Asp Gly Gly Asn Gly Gly Asn Ser Gly
435 440 445

Ala Lys Ala Gly Gly Ala Gly Gly Lys Gly Gln Ala Gly Gln Pro Asn
450 455 460

Ser Gly Thr Glu Pro Gly Phe Gly Gly Asp Gly Gly Leu Gly Gly Ala
465 470 475 480

Gly Ala Thr Pro

<210> 20
<211> 1079
<212> PRT
<213> M. tuberculosis

<220>
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<223> PE_PGRS

<220>
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<223> gi|2924449

<400> 20

Pro Gln Gly Ala Asp Gly Asn Ala Gly Asn Gly Gly Asp Gly Gly Val
1 5 10 15

Gly Gly Asn Gly Gly Asn Gly Ala Asp Asn Thr Thr Thr Ala Ala Ala
20 25 30

Gly Thr Thr Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Thr Gly
35 40 45

Gly Thr Gly Gly Ala Ala Gly Thr Gly Thr Gly Gly Gln Gln Gly Asn
50 55 60

Gly Gly Asn Gly Gly Asn Gly Gly Thr Gly Gly Lys Gly Gly Thr Gly
65 70 75 80

Gly Asp Gly Ala Leu Ala Gly Ser Ser Gly Gly Ala Gly Gly Lys Gly
85 90 95

Gly Asn Gly Gly Asp Ala Gly Lys Ala Gly Thr Gly Ser Ala Pro Gly
100 105 110

Thr Ala Gly Thr Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ile
115 120 125

Gly Ala Ala Gly Thr Thr Gly Pro Val Gly Thr Gly Ala Ser Gly Gly
130 135 140

Thr Gly Gly Ser Gly Gly Ala Gly Gly Thr Gly Gly Asp Gly Gly Ala
145 150 155 160

Ala Asn Gly Gly Thr Ala Gly Ala Gly Gly Ala Gly Gly Asn Gly Gly
165 170 175

Lys Gly Gly Asp Gly Gly Ala Gly Val Thr Ser Ser Thr Ala Gly Asn
180 185 190

Ser Gly Gly Ala Gly Gly Ser Gly Gly Lys Gly Gly Asp Ala Gly Ala
195 200 205

Gly Gly Ala Gly Ala Thr Pro Gly Ala Asn Gly Ile Ala Gly Asn Gly
210 215 220

Gly Asp Gly Gly Asp Gly Ala Ala Gly Ala Val Gly Ile Ser Gly Ala
225 230 235 240

Thr Gly Ala Gly Asp Gly Gly His Gly Gly Thr Gly Ala Ala Gly Gly
245 250 255

Asn Gly Gly Thr Gly Gly Ala Gly Gly Ser Gly Ile Asp Gly Val Gly
260 265 270

Gly Gly Thr Gly Gly Thr Gly Gly Asn Gly Gly Asn Gly Ala Ile Gly
275 280 285

Gly Ala Gly Gly Asp Ala Gly Gly Ser Gly Asn Ser Gly Gly Asn Gly
290 295 300

Gly Ile Gly Gly Lys Gly Gly Asn Ala Gly Ala Gly Gly Ala Ala Gly
305 310 315 320

Ser Asn Gly Gly Thr Val Gly Ala Asn Gly Thr Gly Gly Asp Gly Gly
325 330 335

Asn Gly Gly Ala Ala Gly Ala Ala Thr Ala Gly Ser Asn Gly Gly Ala
340 345 350

Gly Thr Gly Ser Ala Gly Gly Asn Gly Gly Thr Gly Gly Arg Gly Gly
355 360 365

Ser Gly Gly Ala Gly Gly Asp Gly Ile Gly Gly Val Gly Gly Gly Lys
370 375 380

Gly Gly Asn Gly Ala Asp Gly Glu Val Gly Gly Ala Gly Gly Ala Gly
385 390 395 400

Gly Ser Gly Pro Asn Thr Ser Pro Gly Gly Asn Gly Gly Gln Gly Gly
405 410 415

Gln Gly Gly Ser Gly Gly Ala Gly Gly Ala Ala Gly Ala Gly Gly Ala
420 425 430

Gly Gly Gly Ala Asn Gly Thr Ala Gly Asn Gly Gly Gln Gly Gly Ala
435 440 445

Gly Gly Thr Gly Gly Ala Gly Ala Ala Ser Ser Ala Thr Asn Gly Gly
450 455 460

Ser Gly Gly Ala Gly Gly Thr Gly Gly Asp Gly Gly Ser Gly Gly Ala
465 470 475 480

Gly Gly Thr Gly Gly Ala Gly Gly Thr Gly Gly Ala Ala Gly Asp Gly
485 490 495

Gly Gln Gly Gly Gln Gly Gly Ala Gly Gly Gly Ala Gly Gly Gln Gly
500 505 510

Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Asn Gly Gly Asn Ile Thr
515 520 525

Gly Gly Thr Ala Gly Thr Ala Gly Ala Ala Gly Asn Gly Gly Ala Ala
530 535 540

Gly Lys Gly Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Thr Gly
545 550 555 560

Gly Gln Gly Gly Ala Gly Gly Asp Gly Gly Ala Gly Gly Thr Gly Gly
565 570 575

Asp Arg Thr Val Gly Gly Gly Thr Val Pro Ala Gly Ser Gly Gly Gln
580 585 590

Gly Gly Asn Ala Gly Gly Gly Gly Ala Gly Gly Gln Gly Gly Ala Asp
595 600 605

Gly Gly Ser Gly Gly Asp Gly Gly Asp Ala Gly Thr Gly Gly Asn Gly
610 615 620

Gly Asn Gly Gly Asn Arg Asn Ser Gly Asn Gly Thr Gly Gly Ala Gly
625 630 635 640

Gly Asn Gly Gly Gly Gly Ala Asn Gly Gly Ala Gly Gly Ala Gly Gly
645 650 655

Ser Gly Gly Gly Thr Gly Gly Asn Gly Gly Ala Gly Gly Asp Ala Gly
660 665 670

Asp Ala Gly Asn Gly Gly Asn Gly Asn Gly Thr Gly Asn Gly Gly Asn
675 680 685

Gly Gly Asn Gly Gly Ile Ala Gly Met Gly Gly Asn Gly Gly Ala Gly
690 695 700

Thr Gly Ser Gly Asn Gly Gly Asn Gly Gly Ser Gly Gly Asn Gly Gly
705 710 715 720

Asn Ala Gly Met Gly Gly Asn Ser Gly Thr Gly Ser Gly Asp Gly Gly
725 730 735

Ala Gly Gly Asn Gly Gly Ala Ala Gly Thr Gly Gly Thr Gly Gly Asp
740 745 750

Gly Gly Leu Thr Gly Thr Gly Gly Thr Gly Gly Ser Gly Gly Thr Gly
755 760 765

Gly Asp Gly Gly Asn Gly Gly Asn Gly Ala Asp Asn Thr Ala Asn Met
770 775 780

Thr Ala Gln Ala Gly Gly Asp Gly Gly Asn Gly Gly Asp Gly Gly Phe
785 790 795 800

Gly Gly Gly Ala Gly Ala Gly Gly Gly Gly Leu Thr Ala Gly Ala Asn
805 810 815

Gly Thr Gly Gly Gln Gly Gly Ala Gly Gly Asp Gly Gly Asn Gly Ala
820 825 830

Ile Gly Gly His Gly Pro Leu Thr Asp Asp Pro Gly Gly Asn Gly Gly
835 840 845

Thr Gly Gly Asn Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Ile Gly
850 855 860

Ser Leu Gly Gly Gly Thr Gly Gly Asp Gly Gly Asn Gly Gly Asn Gly
865 870 875 880

Gly Thr Gly Gly Glu Gly Gly Glu Val Gly Gly Ala Gly Gly Thr Gly
885 890 895

Gly Ala Ala Gly Asn Gly Gly Asp Gly Gly Thr Gly Gly Thr Gly Gly
900 905 910

Gly Asp Gly Gly Ala Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly
915 920 925

Leu Gly Asp Pro Arg Val Gly Gly Ser Gly Gly Asp Gly Gly Thr Gly
930 935 940

Gly Ser Gly Gly Ala Ala Gly Asn Gly Gly Asn Gly Gly Asn Ala Gly
945 950 955 960

Ala Gly Gly Asn Gly Asn Gly Gly Thr Gly Gly Ala Gly Gly Ile Gly
965 970 975

Gly Thr Gly Gly Asn Gly Gly Asp Ala Glu Pro Gly Val Pro Pro Gly
980 985 990

Ala Gly Gly Ala Gly Gly Ala Gly Thr Thr Gly Gly Lys Gly Gly Thr
995 1000 1005

Gly Gly Asn Gly Ser Gly Thr Gly Ser Gly Gly Thr Gly Gly Asp
1010 1015 1020

Gly Gly Thr Gly Gly Gly Gly Gly Asn Gly Gly Thr Gly Trp Asn
1025 1030 1035

Gly Gly Lys Gly Asp Thr Gly Ser Gly Gly Gly Ala Gly Asp Gly
1040 1045 1050

Gly Lys Ala Pro Ala Gly Gly Thr Gly Gly Ala Gly Gly Asp Gly
1055 1060 1065

Gly Ala Gly Gly Lys Gly Gly Ser Gly Gly Val
1070 1075

<210> 21
<211> 354
<212> PRT
<213> M. tuberculosis

<220>
<221> misc_feature
<223> PPE

<220>

<221> misc_feature

<223> gi|1781260

<400> 21

Met Pro Gly Arg Phe Arg Asn Phe Gly Ser Gln Asn Leu Gly Ser Gly
1 5 10 15

Asn Ile Gly Ser Thr Asn Val Gly Ser Gly Asn Ile Gly Ser Thr Asn
20 25 30

Val Gly Ser Gly Asn Ile Gly Asp Thr Asn Phe Gly Asn Gly Asn Asn
35 40 45

Gly Asn Phe Asn Phe Gly Ser Gly Asn Thr Gly Ser Asn Asn Ile Gly
50 55 60

Phe Gly Asn Thr Gly Ser Gly Asn Phe Gly Phe Gly Asn Thr Gly Asn
65 70 75 80

Asn Asn Ile Gly Ile Gly Leu Thr Gly Asp Gly Gln Ile Gly Ile Gly
85 90 95

Gly Leu Asn Ser Gly Ser Gly Asn Ile Gly Phe Gly Asn Ser Gly Thr
100 105 110

Gly Asn Val Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Phe Gly
115 120 125

Asn Ser Gly Thr Ala Asn Thr Gly Phe Gly Asn Ala Gly Asn Val Asn
130 135 140

Thr Gly Phe Trp Asn Gly Gly Ser Thr Asn Thr Gly Leu Ala Asn Ala
145 150 155 160

Gly Ala Gly Asn Thr Gly Phe Phe Asp Ala Gly Asn Tyr Asn Phe Gly
165 170 175

Ser Leu Asn Ala Gly Asn Ile Asn Ser Ser Phe Gly Asn Ser Gly Asp
180 185 190

Gly Asn Ser Gly Phe Leu Asn Ala Gly Asp Val Asn Ser Gly Val Gly
195 200 205

Asn Ala Gly Asp Val Asn Thr Gly Leu Gly Asn Ser Gly Asn Ile Asn
210 215 220

Thr Gly Gly Phe Asn Pro Gly Thr Leu Asn Thr Gly Phe Phe Ser Ala
 225 230 235 240

Met Thr Gln Ala Gly Pro Asn Ser Gly Phe Phe Asn Ala Gly Thr Gly
 245 250 255

Asn Ser Gly Phe Gly His Asn Asp Pro Ala Gly Ser Gly Asn Ser Gly
 260 265 270

Ile Gln Asn Ser Gly Phe Gly Asn Ser Gly Tyr Val Asn Thr Ser Thr
 275 280 285

Thr Ser Met Phe Gly Gly Asn Ser Gly Val Leu Asn Thr Gly Tyr Gly
 290 295 300

Asn Ser Gly Phe Tyr Asn Ala Ala Val Asn Asn Thr Gly Ile Phe Val
 305 310 315 320

Thr Gly Val Met Ser Ser Gly Phe Phe Asn Phe Gly Thr Gly Asn Ser
 325 330 335

Gly Leu Leu Val Ser Gly Asn Gly Leu Ser Gly Phe Phe Lys Asn Leu
 340 345 350

Phe Gly

<210> 22
 <211> 29
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> misc_feature
 <223> KdpF protein

<220>
 <221> misc_feature
 <223> gi|9947600

<400> 22

Met Thr Val Leu Asp Trp Leu Ser Leu Ala Leu Ala Thr Gly Leu Phe
 1 5 10 15

Val Tyr Leu Leu Val Ala Leu Leu Arg Ala Asp Arg Ala
 20 25

<210> 23
 <211> 352
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> misc_feature
 <223> alginate regulatory protein AlgP

<220>
 <221> misc_feature
 <223> gi|9951563

<400> 23

Met Ser Ala Asn Lys Lys Pro Val Thr Thr Pro Leu His Leu Leu Gln
 1 5 10 15

Gln Leu Ser His Ser Leu Val Glu His Leu Glu Gly Ala Cys Lys Gln
 20 25 30

Ala Leu Val Asp Ser Glu Lys Leu Leu Ala Lys Leu Glu Lys Gln Arg
 35 40 45

Gly Lys Ala Gln Glu Lys Leu His Lys Ala Arg Thr Lys Leu Gln Asp
 50 55 60

Ala Ala Lys Ala Gly Lys Thr Lys Ala Gln Ala Lys Ala Arg Glu Thr
 65 70 75 80

Ile Ser Asp Leu Glu Glu Ala Leu Asp Thr Leu Lys Ala Arg Gln Ala
 85 90 95

Asp Thr Arg Thr Tyr Ile Val Gly Leu Lys Arg Asp Val Gln Glu Ser
 100 105 110

Leu Lys Leu Ala Gln Gly Val Gly Lys Val Lys Glu Ala Ala Gly Lys
 115 120 125

Ala Leu Glu Ser Arg Lys Ala Lys Pro Ala Thr Lys Pro Ala Ala Lys
 130 135 140

Ala Ala Ala Lys Pro Ala Val Lys Thr Val Ala Ala Lys Pro Ala Ala
 145 150 155 160

Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala
 165 170 175

Lys Thr Ala Ala Ala Lys Pro Ala Ala Lys Pro Thr Ala Lys Pro Ala
 180 185 190
 Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Thr Ala Ala Ala Lys Pro
 195 200 205
 Ala Ala Lys Pro Ala Ala Lys Pro Val Ala Lys Pro Ala Ala Lys Pro
 210 215 220
 Ala Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys
 225 230 235 240
 Pro Val Ala Lys Pro Thr Ala Lys Pro Ala Ala Lys Thr Ala Ala Ala
 245 250 255
 Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala
 260 265 270
 Lys Pro Val Ala Lys Ser Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala
 275 280 285
 Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Val
 290 295 300
 Ala Ala Lys Pro Ala Ala Thr Lys Pro Ala Thr Ala Pro Ala Ala Lys
 305 310 315 320
 Pro Ala Ala Thr Pro Ser Ala Pro Ala Ala Ala Ser Ser Ala Ala Ser
 325 330 335
 Ala Thr Pro Ala Ala Gly Ser Asn Gly Ala Ala Pro Thr Ser Ala Ser
 340 345 350

<210> 24
 <211> 309
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> misc_feature
 <223> polyhydroxyalkanoate synthesis protein PhaF

<220>
 <221> misc_feature
 <223> gi|9951352

<400> 24

Met Ala Gly Lys Lys Lys Ser Glu Lys Glu Ser Ser Trp Ile Gly Glu
 1 5 10 15
 Ile Glu Lys Tyr Ser Arg Gln Ile Trp Leu Ala Gly Leu Gly Ala Tyr
 20 25 30
 Ser Lys Val Ser Lys Asp Gly Ser Lys Leu Phe Glu Thr Leu Val Lys
 35 40 45
 Asp Gly Glu Lys Ala Glu Lys Glu Ala Lys Ser Asp Val Asp Ala Gln
 50 55 60
 Val Gly Ala Ala Lys Ala Ser Ala Arg Ser Ala Lys Ser Lys Val Asp
 65 70 75 80
 Glu Val Arg Asp Arg Ala Leu Gly Lys Trp Ser Glu Leu Glu Glu Ala
 85 90 95
 Phe Asp Lys Arg Leu Asn Ser Ala Ile Ser Arg Leu Gly Val Pro Ser
 100 105 110
 Arg Asn Glu Val Lys Glu Leu His Ser Lys Val Asp Thr Leu Thr Lys
 115 120 125
 Gln Ile Glu Lys Leu Thr Gly Val Ser Val Lys Pro Ala Ala Lys Ala
 130 135 140
 Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Thr
 145 150 155 160
 Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Ala Ala Lys
 165 170 175
 Pro Ala Ala Lys Pro Ala Ala Lys Lys Thr Ala Ala Lys Thr Ala Ala
 180 185 190
 Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Thr Ala Lys Ala Ala
 195 200 205
 Ala Lys Pro Ala Thr Lys Pro Ala Ala Lys Ala Ala Ala Lys Pro Ala
 210 215 220
 Ala Lys Pro Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro
 225 230 235 240

Ala Ala Ala Thr Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro
245 250 255

Ala Ala Lys Lys Pro Ala Ala Lys Lys Pro Ala Ala Lys Pro Ala Ala
260 265 270

Ala Lys Pro Ala Ala Pro Ala Ala Ser Ser Ser Ala Pro Ala Ala Pro
275 280 285

Ala Ala Thr Pro Ala Ala Ser Ala Pro Ala Ala Asn Ala Pro Ala Thr
290 295 300

Pro Ser Ser Gln Gly
305

<210> 25
<211> 632
<212> PRT
<213> T. pallidum

<220>
<221> misc_feature
<223> dicarboxylate transporter (dctM)

<220>
<221> misc_feature
<223> gi|3323280

<400> 25

Met Lys Gly Thr Arg Gly Gln Leu Val Leu Arg Ser Ile Ala Leu Leu
1 5 10 15

Leu Ile Gly Thr Leu Met Leu Leu Pro Leu Val Leu Phe Leu Ile Glu
20 25 30

Arg Ile Phe Gly Phe Leu Thr Arg Gly Val Gly Ser Glu Val Phe Ser
35 40 45

Ala His Glu Asp Phe Ile Phe Leu Phe Phe Ser Ser Ser Asp Ala Ala
50 55 60

Val Ala Gln Leu Ala Phe Val Phe Ser Cys Val Ala Gly Ile Tyr Ala
65 70 75 80

Ala Arg Glu Arg Lys His Leu Ser Val Thr Leu Phe Ser Cys Asp Val
85 90 95

Asp Arg Pro Met His Arg Val Leu Ser Phe Leu Ser Ala Ile Cys Thr
 100 105 110

Val Ala Val Leu Ser Ala Cys Phe Phe Ala Ser Gly Pro Asn Ile Val
 115 120 125

Ala Val Phe Arg Lys Glu Glu Ala Val Trp Gly Val Pro Leu Arg Trp
 130 135 140

Ile Phe Thr Ala Leu Pro Cys Met Tyr Gly Ala Leu Leu Phe His Tyr
 145 150 155 160

Ala Arg Glu Val Lys Cys Arg Thr Cys Val Ile Val Gly Leu Leu Val
 165 170 175

Gly Val Leu Ile Ser Thr Gly Ser Ile Ala Ser Val Leu Phe His Leu
 180 185 190

Phe Asp Leu Thr Val Pro Leu Leu Asp Ser Val Phe His Gly Trp Val
 195 200 205

Ala Val Gly Thr Arg Leu Phe Trp Pro Phe Val Leu Leu Leu Leu Leu
 210 215 220

Leu Ala Ala Gln Gly Leu Pro Leu Phe Ile Thr Leu Leu Ala Ile Ala
 225 230 235 240

Tyr Leu Ala Leu Ser Val Asp Gly Gly Tyr Val Asp Thr Leu Pro Leu
 245 250 255

Glu Gly Tyr Lys Ile Leu Thr Asp Thr Gly Gly Ile Val Ala Val Pro
 260 265 270

Leu Phe Ala Thr Ala Ser Leu Leu Leu Ala Arg Gly Ser Thr Gly Thr
 275 280 285

Arg Leu Leu Arg Leu Val Lys Glu Ala Val Gly Trp Leu Arg Gly Gly
 290 295 300

Ala Ala Val Ala Cys Val Ala Val Ala Ala Leu Phe Thr Ser Leu Thr
 305 310 315 320

Gly Val Ser Gly Val Thr Ile Leu Ala Leu Gly Ser Leu Phe Lys Leu
 325 330 335

Ile Leu Thr Gly Asn Lys Tyr Pro Glu His Asp Ala Glu Ala Leu Ile
340 345 350

Thr Ser Ser Gly Ala Ile Gly Leu Leu Phe Pro Pro Ser Ala Ala Ile
355 360 365

Ile Ile Phe Gly Ala Thr Asn Ile Leu Thr Val His Ile Val Asp Leu
370 375 380

Phe Lys Gly Ala Leu Leu Pro Gly Thr Leu Leu Val Leu Ser Ala Met
385 390 395 400

Cys Leu Gly Val Ala Lys Asp Arg Thr Gln Val Arg Pro Ser Phe Ser
405 410 415

Trp Gln Leu Leu Val His Ala Val Arg Gly Ser Val Phe Asp Leu Ala
420 425 430

Leu Pro Val Cys Ile Ser Leu Gly Tyr Phe Ser Gly Thr Leu Asn Leu
435 440 445

Leu Gln Cys Ala Ser Leu Thr Thr Leu Leu Ala Phe Val Leu Gly Thr
450 455 460

Trp Val Arg Arg Asp Phe Thr Val Lys Glu Ala Cys Ala Thr Ala Leu
465 470 475 480

Glu Ser Leu Pro Ile Val Gly Gly Ile Leu Ile Ile Val Ala Ala Ala
485 490 495

Lys Gly Leu Ser Phe Tyr Leu Val Asp Ala Asn Val Pro Asp Thr Leu
500 505 510

Ile Ala Phe Leu Gln His Ala Ile Ser Ser Lys Tyr Ala Phe Leu Leu
515 520 525

Leu Leu Asn Val Leu Leu Leu Gly Val Gly Cys Ile Met Asp Leu Tyr
530 535 540

Ser Ala Ile Leu Val Ile Ser Pro Leu Val Leu Pro Leu Ala Val His
545 550 555 560

Phe Gly Val His Pro Val His Ala Ser Val Val Phe Leu Met Asn Leu
565 570 575

Glu Leu Gly Ala Leu Thr Pro Pro Ile Gly Met Asn Leu Phe Ile Ala
580 585 590

Ser Phe Ala Phe Glu Lys Pro Ile Val Tyr Leu Thr Arg Ala Ile Ala
595 600 605

Pro Phe Leu Leu Ala Gln Leu Gly Val Leu Leu Leu Thr Thr Tyr Ile
610 615 620

Pro Trp Leu Ser Thr Ala Phe Leu
625 630

<210> 26
<211> 653
<212> PRT
<213> Vibrio cholerae

<220>
<221> misc_feature
<223> iron(III) ABC transporter, permease protein

<220>
<221> misc_feature
<223> gi|9654609

<400> 26

Met Ser Val Leu Arg Leu Thr Gly Leu Gly Ala Leu Thr Leu Leu Leu
1 5 10 15

Ala Leu Val Ser Leu Gln Trp Gly His Asn Leu Thr Leu Asn Glu Gln
20 25 30

Trp Gln Leu Val Leu Gly His Gln Ala Ala Gln Ser Phe Ala Gln Val
35 40 45

Asn Phe Ile Tyr Ala Gln Leu Pro Arg Ala Val Met Ala Ile Val Val
50 55 60

Gly Ala Val Leu Gly Leu Val Gly Ser Leu Met Gln Gln Leu Thr Gln
65 70 75 80

Asn Arg Leu Thr Ser Pro Leu Thr Leu Gly Thr Ser Ser Gly Ala Trp
85 90 95

Leu Gly Leu Ile Ile Val Asn Ile Trp Phe Ser Asp Trp Val Ala Asp
100 105 110

Tyr Ser Ala Leu Ala Ala Met Ala Gly Ala Leu Leu Ala Phe Ala Leu
115 120 125

Ile Ile Ser Ile Ala Gly Leu Arg Asn Leu Thr Gly Leu Pro Leu Val
130 135 140

Val Ser Gly Met Val Val Asn Ile Leu Leu Gly Ser Ile Ala Thr Ala
145 150 155 160

Leu Val Leu Leu Asn Glu Glu Phe Ala Gln Asn Val Phe Met Trp Gly
165 170 175

Ala Gly Asp Leu Ala Gln Asn Gly Trp Glu Trp Leu Thr Trp Leu Leu
180 185 190

Pro Arg Leu Ala Leu Val Phe Pro Leu Leu Leu Phe Ala Pro Arg Val
195 200 205

Leu Thr Leu Leu Arg Leu Gly His Glu Gly Ala Ala Ala Arg Gly Leu
210 215 220

Ala Val Leu Pro Ala Phe Leu Phe Leu Met Ala Gly Gly Ile Trp Leu
225 230 235 240

Val Ser Ala Ser Ile Thr Ala Val Gly Val Ile Gly Phe Ile Gly Leu
245 250 255

Leu Thr Pro Asn Ile Ala Arg Ser Leu Gly Ala Arg Thr Thr Lys Met
260 265 270

Glu Leu Tyr Ser Ser Ala Leu Leu Gly Ala Leu Leu Leu Leu Ala Thr
275 280 285

Asp Met Leu Ala Met Gly Leu Ser Val Trp Ala Glu Glu Val Val Pro
290 295 300

Ser Gly Ile Thr Ala Ala Val Ile Gly Ala Pro Ala Leu Ile Trp Phe
305 310 315 320

Ser Arg Arg Gln Leu Gln Ala Gln Asp Ser Leu Ser Ile Ser Leu Ser
325 330 335

Ser His Arg Arg Ser Pro Ser Arg Trp Ala Val Met Leu Ile Ala Ala
340 345 350

Ala Leu Leu Leu Ala Leu Ser Leu His Ile Gly Trp Gln Met Glu Ser
355 360 365

Ala Ser Trp Ala Leu Pro Ser Glu Phe Gln Trp Pro Leu Arg Trp Pro
370 375 380

Arg Met Leu Thr Ala Leu Phe Ala Gly Val Gly Leu Ala Ile Ala Gly
385 390 395 400

Thr Leu Leu Gln Arg Leu Ile Tyr Asn Pro Leu Ala Ser Pro Asp Ile
405 410 415

Leu Gly Val Ser Ser Gly Ala Thr Phe Ala Leu Val Phe Ala Ser Leu
420 425 430

Phe Leu Gly Gln Ser Leu Gln Ser Thr His Trp Met Thr Ala Leu Leu
435 440 445

Gly Ser Ala Ala Val Leu Val Ala Leu Leu Leu Leu Gly Arg Arg His
450 455 460

His Tyr Ala Pro Ser Ser Leu Ile Leu Thr Gly Ile Ala Ile Thr Ala
465 470 475 480

Leu Leu Glu Ala Leu Val Gln Phe Thr Leu Ala Lys Gly Thr Gly Asp
485 490 495

Ser Tyr Gln Ile Leu Leu Trp Leu Ser Gly Ser Thr Tyr Arg Ala Thr
500 505 510

Gly Glu Gln Ala Leu Leu Leu Ser Val Gly Val Val Gly Leu Thr Leu
515 520 525

Leu Ala Leu Gly Leu Ser Arg Trp Leu Thr Leu Ile Ser Ile Gly Arg
530 535 540

Gly Phe Ala Ser Ala Arg Gly Leu Ser Ala Ser Arg Ala Ser Leu Val
545 550 555 560

Leu Leu Ile Leu Val Ala Leu Leu Cys Ala Leu Val Thr Ala Thr Met
565 570 575

Gly Pro Val Ser Phe Val Gly Leu Ile Ala Pro His Met Ala Met Met
580 585 590

Leu Gly Ala Gln Arg Ala Pro Ser Gln Leu Leu Leu Ala Ala Leu Val
595 600 605

Gly Gly Thr Leu Met Leu Trp Ala Asp Trp Leu Gly Gln Ala Leu Leu
610 615 620

Phe Pro Ala Gln Ile Ala Ala Gly Thr Leu Val Ala Ile Ile Gly Gly
625 630 635 640

Ser Tyr Phe Leu Leu Leu Leu Leu Ser Gln Arg Ala Arg
645 650

<210> 27
<211> 356
<212> PRT
<213> Vibrio cholerae

<220>
<221> misc_feature
<223> tolA protein

<220>
<221> misc_feature
<223> gi|9656364

<400> 27

Met Lys Glu Asn Lys Ser Arg Lys Ser Asn Asp Ala Lys Ser Ile Thr
1 5 10 15

Ile Ser Leu Ala Met His Gly Ala Leu Val Ala Ile Leu Leu Trp Gly
20 25 30

Ala Asp Phe Thr Met Ser Asp Pro Glu Pro Thr Gly Gln Met Ile Glu
35 40 45

Ala Val Val Ile Asp Pro Gln Leu Val Arg Gln Gln Ala Gln Gln Ile
50 55 60

Arg Ser Gln Arg Glu Glu Ala Ala Lys Lys Glu Gln Glu Arg Leu Asp
65 70 75 80

Lys Leu Arg Arg Glu Ser Glu Gln Leu Glu Lys Asn Arg Gln Ala Glu
85 90 95

Glu Glu Arg Ile Arg Gln Leu Lys Glu Gln Gln Ala Lys Glu Ala Lys
100 105 110

Ala Ala Arg Glu Ala Glu Lys Leu Arg Glu Gln Lys Glu Gln Glu Arg
 115 120 125

Leu Ala Ala Glu Gln Lys Ala Arg Glu Glu Lys Glu Arg Ala Ala Lys
 130 135 140

Ala Glu Ala Glu Arg Lys Val Lys Glu Glu Ala Ala Lys Lys Ala Glu
 145 150 155 160

Gln Glu Arg Val Ala Lys Glu Ala Ala Ala Lys Ala Glu Gln Gln
 165 170 175

Arg Ile Glu Arg Glu Lys Glu Ala Lys Leu Ala Glu Glu Lys Ala Lys
 180 185 190

Arg Glu Lys Glu Val Ala Ala Lys Ala Glu Gln Glu Arg Leu Ala Lys
 195 200 205

Glu Lys Ala Ala Lys Glu Ala Ala Asp Lys Ala Lys Lys Glu Lys Glu
 210 215 220

Arg Ala Ala Lys Ala Glu Ala Glu Arg Lys Ala Gln Glu Ala Ala Leu
 225 230 235 240

Asn Asp Ile Phe Gly Ser Leu Ser Glu Glu Ser Gln Gln Asn Asn Ala
 245 250 255

Ala Arg Gln Gln Phe Val Thr Ser Glu Val Gly Arg Tyr Gly Ala Ile
 260 265 270

Tyr Thr Gln Leu Ile Arg Gln Asn Leu Leu Val Glu Asp Ser Phe Arg
 275 280 285

Gly Lys Gln Cys Arg Val Asn Leu Lys Leu Ile Pro Thr Gly Thr Gly
 290 295 300

Ala Leu Leu Gly Ser Leu Thr Val Leu Asp Gly Asp Ser Arg Leu Cys
 305 310 315 320

Ala Ala Thr Lys Arg Ala Val Ala Gln Val Asn Ser Phe Pro Leu Pro
 325 330 335

Lys Asp Gln Pro Asp Val Val Glu Lys Leu Lys Asn Ile Asn Leu Thr
 340 345 350

Val Ala Pro Glu
355

<210> 28
<211> 73
<212> PRT
<213> L. major

<220>
<221> misc_feature
<223> hydrophilic surface protein 2

<220>
<221> misc_feature
<223> gi|1743289

<400> 28

Met Gly Ser Ser Cys Thr Lys Asp Ser Ala Lys Glu Pro Gln Lys Ser
1 5 10 15

Ala Gly Asn Ile Asp Thr Thr Thr Arg Ser Asp Glu Lys Asp Gly Val
20 25 30

Leu Val Gln Gln Asn Asp Gly Asp Val Gln Lys Lys Ser Glu Asp Gly
35 40 45

Asp Asn Val Gly Glu Gly Gly Lys Gly Asn Glu Asp Gly Asn Asp Asp
50 55 60

Gln Pro Lys Glu His Ala Ala Gly Asn
65 70

<210> 29
<211> 177
<212> PRT
<213> L. major

<220>
<221> misc_feature
<223> hydrophilic surface protein

<220>
<221> misc_feature
<223> gi|468328

<400> 29

Met Gly Ser Ser Cys Thr Lys Asp Ser Ala Lys Glu Pro Gln Lys Ser
1 5 10 15

Ala Asp Lys Ile Lys Ser Thr Asn Glu Thr Asn Gln Gly Gly Asn Ala
20 25 30

Ser Gly Ser Arg Lys Ser Ala Gly Gly Arg Ala Asn Glu Tyr Asp Pro
35 40 45

Lys Asp Asp Gly Phe Thr Pro Asn Asn Glu Asp Arg Cys Pro Lys Glu
50 55 60

Asp Gly His Ala Pro Lys Asn Asp Asp His Ala Pro Lys Glu Asp Gly
65 70 75 80

His Ala Pro Lys Asn Asp Asp His Ala Pro Lys Glu Asp Gly His Ala
85 90 95

Pro Lys Asn Asp Asp His Ala Pro Lys Glu Asp Gly His Ala Pro Lys
100 105 110

Asn Asp Asp His Ala Pro Lys Glu Asp Gly His Ala Pro Lys Asn Asp
115 120 125

Asp His Ala Pro Lys Glu Asp Gly His Ala Pro Lys Asn Asp Gly Asp
130 135 140

Val Gln Lys Lys Ser Glu Asp Gly Asp Asn Val Gly Glu Gly Gly Lys
145 150 155 160

Gly Asn Glu Asp Gly Asn Asp Asp Gln Pro Lys Glu His Ala Ala Gly
165 170 175

Asn

<210> 30
<211> 106
<212> PRT
<213> Plasmodium falciparum

<220>
<221> misc_feature
<223> predicted integral membrane protein

<220>
<221> misc_feature
<223> gi|3845179

<400> 30

Met Tyr Ile Cys Phe Phe Phe Phe Phe Phe Phe Leu Val Ile Lys Leu
1 5 10 15

Gly Glu Asp Glu Asn Phe Gly Ser Ser Cys Phe Tyr Ser Leu Gly Asn
20 25 30

Thr Lys Ile Leu Thr Thr Val Tyr Gly Pro Asn Pro Asp Ser Lys Tyr
35 40 45

Ala Thr Tyr Ser Lys Gly Lys Val Phe Leu Asp Val Lys Ser Leu Asn
50 55 60

Ile Asn Thr Ile Gly Ala Ser Asp Arg Val Leu Tyr Ile Tyr Gly Phe
65 70 75 80

Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Ile Leu Asn Arg Ser Tyr
85 90 95

Phe Phe Leu Val Leu Phe Ile Ile Phe Ile
100 105

<210> 31
<211> 396
<212> PRT
<213> Plasmodium falciparum

<220>
<221> misc_feature
<223> Circumsporozoite (CS) protein

<220>
<221> misc_feature
<223> gi|4493889

<400> 31

Met Arg Lys Leu Ala Ile Leu Ser Val Ser Ser Phe Leu Phe Val Glu
1 5 10 15

Ala Leu Phe Gln Glu Tyr Gln Cys Tyr Gly Ser Ser Ser Asn Thr Arg
20 25 30

Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Thr Asn Leu Tyr Asn
35 40 45

Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser Leu
50 55 60

Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn Glu
65 70 75 80

Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln Pro
85 90 95

Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn
100 105 110

Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn
115 120 125

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
130 135 140

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
145 150 155 160

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
165 170 175

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
180 185 190

Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
195 200 205

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
210 215 220

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
225 230 235 240

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
245 250 255

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
260 265 270

Lys Asn Asn Gln Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp Pro
275 280 285

Asn Arg Asn Val Asp Glu Asn Ala Asn Ala Asn Ser Ala Val Lys Asn
290 295 300

Asn Asn Asn Glu Glu Pro Ser Asp Lys His Ile Lys Glu Tyr Leu Asn
 305 310 315 320

Lys Ile Gln Asn Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val Thr
 325 330 335

Cys Gly Asn Gly Ile Gln Val Arg Ile Lys Pro Gly Ser Ala Asn Lys
 340 345 350

Pro Lys Asp Glu Leu Asp Tyr Ala Asn Asp Ile Glu Lys Lys Ile Cys
 355 360 365

Lys Met Glu Lys Cys Ser Ser Val Phe Asn Val Val Asn Ser Ser Ile
 370 375 380

Gly Leu Ile Met Val Leu Ser Phe Leu Phe Leu Asn
 385 390 395

<210> 32
 <211> 497
 <212> PRT
 <213> B. burgdorferi

<220>
 <221> misc_feature
 <223> predicted coding region BB0553

<220>
 <221> misc_feature
 <223> gi|2688482

<220>
 <221> misc_feature
 <222> (198)..(198)
 <223> "Xaa" may be any amino acid

<400> 32

Met Asn Lys Thr Lys Asn Arg Ser Leu Thr Tyr Phe Ile Ile Leu Ser
 1 5 10 15

Cys Ile Ser Leu Phe Gly Ala Asn Asn Asn Thr Ile Ser Tyr Ser Ser
 20 25 30

Ile Glu Ile Pro Leu Glu Asp Leu Ser Glu Glu Phe Lys Ser Ser Gly
 35 40 45

Asn Lys Ser Asp Gln Ile Asn Thr Ser Lys His Leu Asn Lys Asn Ile
 50 55 60

Val Ser Tyr Glu Asp Pro Lys Lys Gly Lys Asp Leu Lys Leu Pro Glu
 65 70 75 80

Asn Ile Arg Asp Lys Lys Leu Pro Gln Lys Arg Met Asp Glu Asn Asp
 85 90 95

Leu Lys Ser Val Ile Glu Asn Tyr Glu Asn Lys Ile Lys Asn Ile Glu
 100 105 110

Lys Leu Leu Lys Thr Lys Asn Gln Lys Thr Ser Glu Asn Glu Asn Lys
 115 120 125

Lys Ile Glu Ser Ile Glu Lys Lys Ala Lys Lys Tyr Glu Ile Leu Thr
 130 135 140

Asn Lys Leu Lys Asn Glu Ile Val Glu Ile Lys Lys Leu Leu Asn Lys
 145 150 155 160

Lys Ile Lys Pro Lys Glu Asp Glu Asn Tyr Glu Lys Ile Asn Ile Glu
 165 170 175

Asn Ile Glu Glu Glu Thr Asp Asp Asp Phe Glu Asp Asn Tyr Glu Tyr
 180 185 190

Asn Asp Glu Ile Glu Xaa Thr Asn Glu Asp Asn Tyr Pro Ser Asn Glu
 195 200 205

Gly Ile Ile Asn Asn Leu Lys Glu Asn Leu Asn Glu Asn Glu Lys Tyr
 210 215 220

Tyr Ala Ile Asn Glu Lys Lys Ile Asp Glu Leu Glu Asp Arg Ile Asn
 225 230 235 240

Glu Asn Glu Asn Thr Ile Leu Asp Leu Gln Arg Glu Leu Arg Asn Phe
 245 250 255

Lys Lys Lys Asp Asn Ser Asp Lys Asn Leu Glu Glu Ile Glu Glu Asn
 260 265 270

Leu Ser Ser Ile Gly Arg Ile Ile Asn Asp Leu Lys Arg Lys Ile Ser
 275 280 285

Ala Asn Glu Ala Ile Asn Lys Glu Asn Gln Lys Lys Ile Arg Thr Asp
 290 295 300

Lys His Lys Leu Lys Glu Leu Glu Asp Lys Ile Lys Glu Asn Glu Glu
 305 310 315 320

Thr Ile Leu Lys Leu Gln Lys Glu Leu Asn Asn Phe Lys Lys Lys Glu
 325 330 335

Ile Tyr Gln Lys Pro Leu Asn Glu Glu Thr Phe Thr Pro Ser Ile Thr
 340 345 350

Ser Lys Asn Asp Asp Leu Glu Glu Asn Lys Lys Leu Lys Lys Glu Tyr
 355 360 365

Leu Lys Pro Ile Glu Lys Lys Glu Ser Arg Asp Leu Glu Glu Asn Thr
 370 375 380

Lys Ser Thr Pro Lys Thr Thr Met Ile Lys Thr Ala Asp Phe Gln Ile
 385 390 395 400

Tyr Pro Asp Ile Tyr Leu Asn Asn Tyr Lys Phe Lys Glu Lys Gly Asp
 405 410 415

Gln Phe Ala Phe Lys Lys Glu Asn Thr Tyr Tyr Ile Glu Ile Asp Pro
 420 425 430

Thr Asn Asn Leu Asn Glu Ala Leu Lys Asn His Glu Ile Ile Ser Lys
 435 440 445

Tyr Lys Phe Glu Lys Tyr Phe Ile Asn Pro Ile Leu Lys Asn Lys Glu
 450 455 460

Glu Phe Phe Arg Asn Leu Ile Glu Val Lys Asn Ile His Glu Leu Gly
 465 470 475 480

Ile Met Tyr Lys Asn Leu Lys Pro Glu Phe Lys Gln Ile Lys Ile Ile
 485 490 495

Lys

<210> 33
 <211> 31
 <212> PRT
 <213> B. burgdorferi

<220>
<221> misc_feature
<223> predicted coding region BB0148

<220>
<221> misc_feature
<223> gi|2688046

<400> 33

Met Pro Val Lys Lys Asn Ser Thr Lys Ile Lys Lys Lys Glu Thr Gln
1 5 10 15

Ile Ala Ile Ala Leu Lys Ile Ile Ile Ile Tyr Phe Phe Asp
20 25 30

<210> 34
<211> 30
<212> PRT
<213> B. burgdorferi

<220>
<221> misc_feature
<223> predicted coding region BB0150

<220>
<221> misc_feature
<223> gi|2688045

<400> 34

Met Phe Gly Cys Leu Arg Ile His Val Phe Lys Ile Tyr Phe Ile Phe
1 5 10 15

Leu Ile Ile His Tyr Ile Leu Phe Ser Ile Leu Leu Met Ile
20 25 30

<210> 35
<211> 344
<212> PRT
<213> B. burgdorferi

<220>
<221> misc_feature
<223> predicted coding region BB0212

<220>
<221> misc_feature
<223> gi|2688103

<400> 35

Met Met Lys Lys Ile Lys Ser Glu Ile Asn Leu Leu Lys Ile Glu Lys
1 5 10 15

Asp Lys Asn Leu Ile Glu Leu Gly Lys Ile Leu Lys Asn Asn Asn Ile
20 25 30

Val Glu Leu Lys Asn Leu Asn His Tyr Pro Asn Leu Lys Leu Val Glu
35 40 45

Lys Glu Leu Tyr Gln Met Lys Ser Asn Leu Ser Lys Ser Glu Glu Asn
50 55 60

Glu Asn Ile Leu Lys Asn Leu Asn Lys Lys Ile Tyr Ile Leu Lys Lys
65 70 75 80

Glu Tyr Lys Ser Thr Ser Lys Ser Tyr Lys Lys Asn Leu Lys Glu Ile
85 90 95

Ala Lys Thr Ile Ile Glu Ile Tyr Pro Gln Asn Leu Glu Leu Ile Ser
100 105 110

Lys Tyr Asn Met Asn Phe Ser Lys Leu Lys Leu Glu Lys Tyr Lys Lys
115 120 125

Ile Glu Leu Ala Ser Asp His Lys Thr Lys Asn Tyr Leu Gln Arg Ile
130 135 140

Met Leu Glu Val Ser Ser Thr Ile Asn Asn Ile Ile Asn Met Ile Asn
145 150 155 160

Val Tyr Lys Ile Ser Lys Glu Phe Glu Lys Gln Val Phe Thr Lys Tyr
165 170 175

Tyr Pro Ser Glu Asn Phe Glu Ser Ile Met Asn Glu Phe Ser Leu Asn
180 185 190

Lys Lys Leu Asn Asn Val Ile Val Lys Glu Phe Lys Ile Ile Asn Glu
195 200 205

Ile Lys Thr Asn Ile Lys Asn Ile Lys Glu Glu Ile Lys Glu Ile Ile
210 215 220

Ser Thr Ser Lys Lys Glu Lys Ile Tyr Lys Lys Asn Thr Ile Lys Asn
225 230 235 240

Glu Ile Asn Val Ile Thr Lys Asn Lys Glu Asn Ile Leu Lys Lys Ile
245 250 255

Ala Glu Glu Phe Ile Glu Ile Thr Lys Lys Asp Lys Met Thr Ala Lys
260 265 270

Thr Asn Ala Ile Ser Ser Ile Ile Gln Lys Ile Glu Lys Ile Asn Gln
275 280 285

Lys Ile Leu Asn Leu Asn Asn Asp Leu Ile Lys Ile Thr Lys Gln Glu
290 295 300

Glu Ile Lys Asn Ile Gln Gln Lys Ile Gln Ala Leu Thr Lys Glu Lys
305 310 315 320

Asn Lys Ile Asn Asn Lys Leu Asp Ala Leu Thr Ser Lys Ile Glu Val
325 330 335

Ile Gln Asn Glu Leu Asp Asn Glu
340

<210> 36
<211> 30
<212> PRT
<213> B. burgdorferi

<220>
<221> misc_feature
<223> predicted coding region BB0425

<220>
<221> misc_feature
<223> gi|2688333

<400> 36

Met Glu Asp Glu Arg Arg Glu Glu Leu Ser Lys Val Lys Ser Gln Lys
1 5 10 15

Asn Lys Gln Asn Leu Leu Ile Phe Leu Asn Lys Lys Ile Lys
20 25 30

<210> 37
<211> 32
<212> PRT
<213> B. burgdorferi

<220>
<221> misc_feature
<223> predicted coding region BB0433

<220>
 <221> misc_feature
 <223> gi|2688343

 <400> 37

 Met His Lys Phe Phe Lys Leu Ile Leu Lys Leu Phe Ser Phe Tyr Lys
 1 5 10 15

 Glu Ile Leu Gly Phe Lys Arg Arg Ala Lys Phe Ile Phe Cys Tyr Leu
 20 25 30

<210> 38
 <211> 38
 <212> PRT
 <213> B. burgdorferi

<220>
 <221> misc_feature
 <223> predicted coding region BB0520

<220>
 <221> misc_feature
 <223> gi|2688447

<400> 38

 Met Ser Lys Ser Thr Lys Asn Thr Thr Lys Ser Lys Asn Asp Thr Lys
 1 5 10 15

 Asn Ile Leu Ile Asn Lys Lys Ile Lys Phe Phe Ile Leu Thr Lys Lys
 20 25 30

Tyr Thr Arg Thr Phe Tyr
 35

<210> 39
 <211> 36
 <212> PRT
 <213> B. burgdorferi

<220>
 <221> misc_feature
 <223> predicted coding region BB0609

<220>
 <221> misc_feature
 <223> gi|2688540

<400> 39

 Met Thr Met Ile Ile Ile Ile Phe Tyr Lys Tyr Leu Ile Pro Lys Ser
 1 5 10 15

Ile Lys Asp Lys Asn Asn Lys Ser His Lys Thr Phe Ile Lys Lys Phe
 20 25 30

Ile Ile Lys Tyr
 35

<210> 40
 <211> 31
 <212> PRT
 <213> B. burgdorferi

<220>
 <221> misc_feature
 <223> predicted coding region BB0822

<220>
 <221> misc_feature
 <223> gi|2688768

<400> 40

Met Pro Cys Gly Arg Lys Arg Lys Leu Lys Lys Ile Ser Thr His Lys
 1 5 10 15

Arg Lys Lys Lys Arg Arg Lys Asn Arg His Lys Lys Lys Asn Lys
 20 25 30

<210> 41
 <211> 34
 <212> PRT
 <213> B. burgdorferi

<220>
 <221> misc_feature
 <223> predicted coding region BB0848

<220>
 <221> misc_feature
 <223> gi|2688793

<400> 41

Met Tyr Phe Cys Ile Ile Asp Leu Glu Phe Val Gly Val Leu Pro Tyr
 1 5 10 15

Phe Phe Ile Tyr Lys Phe Gly Glu Phe Tyr Phe Ser Phe Phe Gly Lys
 20 25 30

Trp Arg

<210> 42
<211> 51
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> highly acidic protein

<220>
<221> misc_feature
<223> gi|6967728

<400> 42

Met Ala Tyr Glu Asp Glu Glu Asp Leu Asn Tyr Asp Asp Tyr Glu Asn
1 5 10 15

Glu Asp Glu Glu Tyr Pro Gln Asn His His Lys Asn Tyr Asn Tyr Asp
20 25 30

Asp Asp Asp Tyr Glu Tyr Asp Asp Asp Asn Asn Asp Asp Asp Phe Tyr
35 40 45

Glu Met Asp
50

<210> 43
<211> 41
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> hypothetical protein Cj0344

<220>
<221> misc_feature
<223> gi|6967819

<400> 43

Met Phe Gln Asn Ile Ile Lys Tyr Lys Asp Phe Ile Ile Phe Ile Leu
1 5 10 15

Asn Leu Lys Gln Asn Leu Tyr Leu Leu Ile Lys Ile Asn Leu Asp Phe
20 25 30

Lys Asn Phe His Lys Ser Leu Asn Phe
35 40

<210> 44
<211> 37
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> hypothetical protein Cj0567

<220>
<221> misc_feature
<223> gi|6968034

<400> 44

Met Asp Lys Ile Gln Glu Asn Thr Lys Ile Glu Lys Ala Ile Leu Ala
1 5 10 15

Glu Lys Gln Gln Ile Phe Leu Ile Gln Asn Lys Leu Ser Glu Ile Glu
20 25 30

Lys Asn Ile Lys Glu
35

<210> 45
<211> 74
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> small hydrophobic protein

<220>
<221> misc_feature
<223> gi|6968265

<400> 45

Met Leu Glu Phe Ile Phe Thr Leu Ile Leu Asp Phe Thr Phe Tyr Ser
1 5 10 15

Ile Lys Thr Leu Glu Lys Val Phe Leu Gly Arg Thr Ala Leu Val Ile
20 25 30

Leu Phe Val Val Phe Ile Ala Leu Phe Cys Val Lys Gly Leu Phe Leu
35 40 45

Tyr Ile Leu Leu Ala Leu Glu Leu Phe Leu Leu Leu Tyr Leu Phe Leu
50 55 60

Gly Ile Leu Phe Leu Arg Phe Tyr Lys Ser
65 70

<210> 46
<211> 46
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> very hypothetical protein Cj0974

<220>
<221> misc_feature
<223> gi|6968409

<400> 46

Met Leu Lys Met Ile Lys Ile Gln Lys Val Lys Ser Leu Leu Asp Leu
1 5 10 15

Val Lys Lys Leu Lys Asn Lys Gln Ser Leu Lys Ile Lys Asn Gln Thr
20 25 30

Asn Thr Lys Glu Asn Leu Asn Lys Thr His Tyr Leu Thr Ile
35 40 45

<210> 47
<211> 78
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> very hypothetical protein

<220>
<221> misc_feature
<223> gi|6968423

<400> 47

Met Leu Lys Ile Pro Tyr Phe Ser Phe Leu Lys Leu Asp Phe Glu Ile
1 5 10 15

Tyr His Leu Asn Thr Ser Lys Asn Phe Tyr Gly Phe Phe Ile Leu Tyr
20 25 30

Phe Ser Phe Phe Ile Phe Lys Leu Ile Tyr Lys Phe Ser Lys Ser Asn
35 40 45

Lys Lys Ile Tyr Lys Lys Ile Ile Lys Leu Lys Lys Ile Ile Lys Asp
50 55 60

Asn Lys Tyr Leu Ile Phe Leu Cys Tyr Ile Leu Ile Asn Ile
65 70 75

<210> 48
<211> 30
<212> PRT
<213> C. jejuni

<220>
<221> misc_feature
<223> hypothetical protein Cj0748

<220>
<221> misc_feature
<223> gi|6968200

<400> 48

Met Leu Glu Thr Leu Lys Lys Tyr Ala Glu Asn Gln Gly Ile Glu Asp
1 5 10 15

Asn Tyr Pro Lys Lys Ile Tyr Asn Gln Lys Glu Lys Lys Pro
20 25 30

<210> 49
<211> 168
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> CT670 hypothetical protein

<220>
<221> misc_feature
<223> gi|4377009

<400> 49

Met Ala Lys Tyr Pro Leu Glu Pro Val Leu Ala Ile Lys Lys Asp Arg
1 5 10 15

Val Asp Arg Ala Glu Lys Val Val Lys Glu Lys Arg Arg Leu Leu Glu
20 25 30

Ile Glu Gln Glu Lys Leu Arg Glu Lys Glu Ala Glu Arg Asp Lys Val
35 40 45

Lys Asn His Tyr Met Gln Lys Ile Gln Gln Leu Arg Asp Leu Leu Asp
 50 55 60

Glu Gly Thr Thr Ser Asp Ala Val Leu Gln Ile Lys Ser Tyr Ile Lys
 65 70 75 80

Val Val Ala Val Gln Leu Ser Glu Glu Glu Glu Lys Val Asn Lys Gln
 85 90 95

Lys Glu Val Val Leu Ala Ala Ser Lys Glu Leu Glu Lys Ala Glu Val
 100 105 110

Asn Leu Ala Lys Arg Arg Lys Glu Glu Glu Lys Thr Arg Leu His Lys
 115 120 125

Glu Glu Trp Met Lys Glu Ala Leu Lys Glu Glu Ala Arg Ala Glu Glu
 130 135 140

Lys Glu Gln Asp Glu Met Gly Gln Leu Leu Phe Gln Leu Arg Gln Lys
 145 150 155 160

Lys Lys Arg Glu Ser Gly Gly Ser
 165

<210> 50
 <211> 444
 <212> PRT
 <213> C. pneumoniae CWL029

<220>
 <221> misc_feature
 <223> CT579 hypothetical protein

<220>
 <221> misc_feature
 <223> gi|4377120

<400> 50

Met Thr Ser Gly Val Ser Gly Ser Ser Ser Gln Asp Pro Thr Leu Ala
 1 5 10 15

Ala Gln Leu Ala Gln Ser Ser Gln Lys Ala Gly Asn Ala Gln Ser Gly
 20 25 30

His Asp Thr Lys Asn Val Thr Lys Gln Gly Ala Gln Ala Glu Val Ala
 35 40 45

Ala Gly Gly Phe Glu Asp Leu Ile Gln Asp Ala Ser Ala Gln Ser Thr
 50 55 60

Gly Lys Lys Glu Ala Thr Ser Ser Thr Thr Lys Ser Ser Lys Gly Glu
 65 70 75 80

Lys Ser Glu Lys Ser Gly Lys Ser Lys Ser Ser Thr Ser Val Ala Ser
 85 90 95

Ala Ser Glu Thr Ala Thr Ala Gln Ala Val Gln Gly Pro Lys Gly Leu
 100 105 110

Arg Gln Asn Asn Tyr Asp Ser Pro Ser Leu Pro Thr Pro Glu Ala Gln
 115 120 125

Thr Ile Asn Gly Ile Val Leu Lys Lys Gly Met Gly Thr Leu Ala Leu
 130 135 140

Leu Gly Leu Val Met Thr Leu Met Ala Asn Ala Ala Gly Glu Ser Trp
 145 150 155 160

Lys Ala Ser Phe Gln Ser Gln Asn Gln Ala Ile Arg Ser Gln Val Glu
 165 170 175

Ser Ala Pro Ala Ile Gly Glu Ala Ile Lys Arg Gln Ala Asn His Gln
 180 185 190

Ala Ser Ala Thr Glu Ala Gln Ala Lys Gln Ser Leu Ile Ser Gly Ile
 195 200 205

Val Asn Ile Val Gly Phe Thr Val Ser Val Gly Ala Gly Ile Phe Ser
 210 215 220

Ala Ala Lys Gly Ala Thr Ser Ala Leu Lys Ser Ala Ser Phe Ala Lys
 225 230 235 240

Glu Thr Gly Ala Ser Ala Ala Gly Gly Ala Ala Ser Lys Ala Leu Thr
 245 250 255

Ser Ala Ser Ser Ser Val Gln Gln Thr Met Ala Ser Thr Ala Lys Ala
 260 265 270

Ala Thr Thr Ala Ala Ser Ser Ala Gly Ser Ala Ala Thr Lys Ala Ala
 275 280 285

Ala Asn Leu Thr Asp Asp Met Ala Ala Ala Ala Ser Lys Met Ala Ser
 290 295 300

Asp Gly Ala Ser Lys Ala Ser Gly Gly Leu Phe Gly Glu Val Leu Asn
 305 310 315 320

Lys Pro Asn Trp Ser Glu Lys Val Ser Arg Gly Met Asn Val Val Lys
 325 330 335

Thr Gln Gly Ala Arg Val Ala Ser Phe Ala Gly Asn Ala Leu Ser Ser
 340 345 350

Ser Met Gln Met Ser Gln Leu Met His Gly Leu Thr Ala Ala Val Glu
 355 360 365

Gly Leu Ser Ala Gly Gln Thr Gly Ile Glu Val Ala His His Gln Arg
 370 375 380

Leu Ala Gly Gln Ala Glu Ala Gln Ala Glu Val Leu Lys Gln Met Ser
 385 390 395 400

Ser Val Tyr Gly Gln Gln Ala Gly Gln Ala Gly Gln Leu Gln Glu Gln
 405 410 415

Ala Met Gln Ser Phe Asn Thr Ala Leu Gln Thr Leu Gln Asn Ile Ala
 420 425 430

Asp Ser Gln Thr Gln Thr Thr Ser Ala Ile Phe Asn
 435 440

<210> 51
 <211> 493
 <212> PRT
 <213> C. pneumoniae CWL029

<220>
 <221> misc_feature
 <223> CT578 hypothetical protein

<220>
 <221> misc_feature
 <223> gi|4377121

<400> 51

Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
 1 5 10 15

Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
20 25 30

Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
35 40 45

Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
50 55 60

Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly
65 70 75 80

Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
85 90 95

Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
100 105 110

Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
115 120 125

Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu
130 135 140

Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser
145 150 155 160

Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg
165 170 175

Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr
180 185 190

Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln
195 200 205

Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile
210 215 220

Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu
225 230 235 240

Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val
245 250 255

Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile Val Ala Ala
260 265 270

Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala Gly Ala Ala
275 280 285

Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala Ala Thr
290 295 300

Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln Ala Val Lys
305 310 315 320

Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala Ala Ile Lys
325 330 335

Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr Leu Val Lys
340 345 350

Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val Phe Ala Lys
355 360 365

Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val Ile
370 375 380

Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val Val
385 390 395 400

Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser Glu
405 410 415

Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly Lys Leu Gln
420 425 430

Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln Ala
435 440 445

Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu Met Thr Gln
450 455 460

Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala Ile
465 470 475 480

Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
485 490

<210> 52
<211> 76
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> CT753 hypothetical protein

<220>
<221> misc_feature
<223> gi|4377216

<400> 52

Met Arg Asn Met Glu Ala Lys Lys Ile Lys Glu Leu Ser Lys Glu Ala
1 5 10 15

Gln Leu Leu Lys Lys Leu Arg Glu Lys Ser Arg Val Leu Asp Glu Lys
20 25 30

Asn Lys Arg Lys Ala Trp Val Ala Lys Leu Val Ala Met Pro Glu Ser
35 40 45

Ile Arg Glu Ile Glu Lys Glu Glu Arg Val Glu Thr Pro Gln Leu Phe
50 55 60

Gln Ala Ile Ala Glu Lys Ile Leu Glu Glu Gly Val
65 70 75

<210> 53
<211> 755
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> CT456 hypothetical protein

<220>
<221> misc_feature
<223> gi|4376866

<400> 53

Met Ala Ala Pro Ile Asn Gln Pro Ser Thr Thr Thr Gln Ile Thr Gln
1 5 10 15

Thr Gly Gln Thr Thr Thr Thr Thr Val Gly Ser Leu Gly Glu His
20 25 30

Ser Val Thr Thr Thr Gly Ser Gly Ala Ala Ala Gln Thr Ser Gln Thr
 35 40 45

Val Thr Leu Ile Ala Asp His Glu Met Gln Glu Ile Ala Ser Gln Asp
 50 55 60

Gly Ser Ala Val Ser Phe Ser Ala Glu His Ser Phe Ser Thr Leu Pro
 65 70 75 80

Pro Glu Thr Gly Ser Val Gly Ala Thr Ala Gln Ser Ala Gln Ser Ala
 85 90 95

Gly Leu Phe Ser Leu Ser Gly Arg Thr Gln Arg Arg Asp Ser Glu Ile
 100 105 110

Ser Ser Ser Ser Asp Gly Ser Ser Ile Ser Arg Thr Ser Ser Asn Ala
 115 120 125

Ser Ser Gly Glu Thr Ser Arg Ala Glu Ser Ser Pro Asp Leu Gly Asp
 130 135 140

Leu Asp Ser Leu Ser Gly Ser Glu Arg Ala Glu Gly Ala Glu Gly Pro
 145 150 155 160

Glu Gly Pro Gly Gly Leu Pro Glu Ser Thr Ile Pro His Tyr Asp Pro
 165 170 175

Thr Asp Lys Ala Ser Ile Leu Asn Phe Leu Lys Asn Pro Ala Val Gln
 180 185 190

Gln Lys Met Gln Thr Lys Gly Gly His Phe Val Tyr Val Asp Glu Ala
 195 200 205

Arg Ser Ser Phe Ile Phe Val Arg Asn Gly Asp Trp Ser Thr Ala Glu
 210 215 220

Ser Ile Lys Val Ser Asn Ala Lys Thr Lys Glu Asn Ile Thr Lys Pro
 225 230 235 240

Ala Asp Leu Glu Met Cys Ile Ala Lys Phe Cys Val Gly Tyr Glu Thr
 245 250 255

Ile His Ser Asp Trp Thr Gly Arg Val Lys Pro Thr Met Glu Glu Arg
 260 265 270

Ser Gly Ala Thr Gly Asn Tyr Asn His Leu Met Leu Ser Met Lys Phe
 275 280 285

Lys Thr Ala Val Val Tyr Gly Pro Trp Asn Ala Lys Glu Ser Ser Ser
 290 295 300

Gly Tyr Thr Pro Ser Ala Trp Arg Arg Gly Ala Lys Val Glu Thr Gly
 305 310 315 320

Pro Ile Trp Asp Asp Val Gly Gly Leu Lys Gly Ile Asn Trp Lys Thr
 325 330 335

Thr Pro Ala Pro Asp Phe Ser Phe Ile Asn Glu Thr Pro Gly Gly Gly
 340 345 350

Ala His Ser Thr Ser His Thr Gly Pro Gly Thr Pro Val Gly Ala Thr
 355 360 365

Val Val Pro Asn Val Asn Val Asn Leu Gly Gly Ile Lys Val Asp Leu
 370 375 380

Gly Gly Ile Asn Leu Gly Gly Ile Thr Thr Asn Val Thr Thr Glu Glu
 385 390 395 400

Gly Gly Gly Thr Asn Ile Thr Ser Thr Lys Ser Thr Ser Thr Asp Asp
 405 410 415

Lys Val Ser Ile Thr Ser Thr Gly Ser Gln Ser Thr Ile Glu Glu Asp
 420 425 430

Thr Ile Gln Phe Asp Asp Pro Gly Gln Gly Glu Asp Asp Asn Ala Ile
 435 440 445

Pro Gly Thr Asn Thr Pro Pro Pro Pro Gly Pro Pro Pro Asn Leu Ser
 450 455 460

Ser Ser Arg Leu Leu Thr Ile Ser Asn Ala Ser Leu Asn Gln Val Leu
 465 470 475 480

Gln Asn Val Arg Gln His Leu Asn Thr Ala Tyr Asp Ser Asn Gly Asn
 485 490 495

Ser Val Ser Asp Leu Asn Gln Asp Leu Gly Gln Val Val Lys Asn Ser
 500 505 510

Glu Asn Gly Val Asn Phe Pro Thr Val Ile Leu Pro Lys Thr Thr Gly
515 520 525

Asp Thr Asp Pro Ser Gly Gln Ala Thr Gly Gly Val Thr Glu Gly Gly
530 535 540

Gly His Ile Arg Asn Ile Ile Gln Arg Asn Thr Gln Ser Thr Gly Gln
545 550 555 560

Ser Glu Gly Ala Thr Pro Thr Pro Gln Pro Thr Ile Ala Lys Ile Val
565 570 575

Thr Ser Leu Arg Lys Ala Asn Val Ser Ser Ser Ser Val Leu Pro Gln
580 585 590

Pro Gln Val Ala Thr Thr Ile Thr Pro Gln Ala Arg Thr Ala Ser Thr
595 600 605

Ser Thr Thr Ser Ile Gly Thr Gly Thr Glu Ser Thr Ser Thr Thr Ser
610 615 620

Thr Gly Thr Gly Thr Gly Ser Val Ser Thr Gln Ser Thr Gly Val Gly
625 630 635 640

Thr Pro Thr Thr Thr Thr Arg Ser Thr Gly Thr Ser Ala Thr Thr Thr
645 650 655

Thr Ser Ser Ala Ser Thr Gln Thr Pro Gln Ala Pro Leu Pro Ser Gly
660 665 670

Thr Arg His Val Ala Thr Ile Ser Leu Val Arg Asn Ala Ala Gly Arg
675 680 685

Ser Ile Val Leu Gln Gln Gly Gly Arg Ser Gln Ser Phe Pro Ile Pro
690 695 700

Pro Ser Gly Thr Gly Thr Gln Asn Met Gly Ala Gln Leu Trp Ala Ala
705 710 715 720

Ala Ser Gln Val Ala Ser Thr Leu Gly Gln Val Val Asn Gln Ala Ala
725 730 735

Thr Ala Gly Ser Gln Pro Ser Ser Arg Arg Ser Ser Pro Thr Ser Pro
740 745 750

Arg Arg Lys
755

<210> 54
<211> 221
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> SET Domain protein

<220>
<221> misc_feature
<223> gi|4377196

<400> 54

Met Ser Thr Val Thr Thr Glu Pro Cys Ser Ser Ile His Ile Ser Leu
1 5 10 15

Asn Asn Asp Trp Arg Asp Ser Gln Pro Tyr Ser Leu Asp Arg Ala Ser
20 25 30

Glu Leu Leu His Phe Arg Phe Leu Pro Ser Leu Val Phe Ser Asn Trp
35 40 45

Lys Val Glu Gln Gln Ile Glu Thr Leu Cys His Lys Ser Glu Lys Arg
50 55 60

Arg Leu Ile Ser Pro Leu Ala Lys Trp Leu Gly Lys Leu His Lys Gln
65 70 75 80

Asp Leu Leu Cys Pro Pro Ala Pro Pro Val Ser Val Cys Trp Ile Asn
85 90 95

Ala His Val Gly Tyr Gly Val Phe Ala Arg Asp Glu Ile Ala Pro Trp
100 105 110

Thr Tyr Ile Gly Glu Tyr Thr Gly Ile Leu Arg His Arg Gln Ala Ile
115 120 125

Trp Met Asp Glu Asn Asp Tyr Cys Phe Arg Tyr Pro Met Pro Leu Phe
130 135 140

Thr Leu Arg Tyr Phe Thr Ile Asp Ser Gly Lys Gln Gly Asn Val Thr
145 150 155 160

Arg Phe Ile Asn His Ser Glu Gln Pro Asn Ala Glu Ala Ile Gly Val
165 170 175

Phe Ser Glu Gly Leu Phe His Val Ile Ile Arg Thr Val Ala Pro Ile
180 185 190

Tyr Ala Gly Gln Glu Ile Cys Tyr His Tyr Gly Pro Leu Tyr Trp Lys
195 200 205

His Arg Lys Lys Arg Glu Glu Phe Ile Pro Glu Glu Glu
210 215 220

<210> 55
<211> 98
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|4376483

<400> 55

Met Ser Tyr Pro Asp Ile Ser Asn Val Gln Ala Ser Ser Ile Gln Ser
1 5 10 15

Ala Leu Leu His Lys Thr Ser Asp Gln Ile Gln Gln Lys Arg Cys Phe
20 25 30

Lys Gln Ser Thr Phe Val Ile Leu Ala Val Ser Leu Val Ile Ile Gly
35 40 45

Ser Leu Phe Leu Leu Ala Gly Val Ala Ile Leu Thr Val Phe Ser His
50 55 60

Gly Val Leu Ser Leu Val Phe Gly Val Leu Gly Ile Val Leu Gly Leu
65 70 75 80

Leu Leu Leu Ala Gly Gly Val Gly Leu Leu Val Glu Glu Ala Lys Ser
85 90 95

Leu Leu

<210> 56
<211> 64
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> CT382.1 hypothetical protein

<220>
<221> misc_feature
<223> gi|4376770

<400> 56

Met Ile Lys Gln Ala Cys Lys Phe Tyr Leu Leu Gln Cys Leu Leu Cys
1 5 10 15

Ala Leu Tyr Trp Leu Leu Lys Tyr Cys Arg Lys Leu Leu Lys Gly Thr
20 25 30

Leu His His Ser Glu Glu Thr Leu Tyr Gln Ala Leu Leu Ser Ser Leu
35 40 45

Ile Asp Leu Leu Tyr Gln Leu Lys Gln Leu Pro Ala Pro Thr Asn Glu
50 55 60

<210> 57
<211> 50
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|4376779

<400> 57

Met Arg Thr Tyr Thr Arg Ser Pro Lys Gln Ser Gly Val Glu Arg Lys
1 5 10 15

Gln Glu Asp Ala Glu Thr Ser Phe Ile Glu Thr Pro Lys Gly Ile Leu
20 25 30

Lys Lys Pro Gly Asn Lys Asp Pro Lys Gly Lys His Val His Trp Lys
35 40 45

Asp Ser
50

<210> 58
<211> 775
<212> PRT
<213> C. pneumoniae CWL029

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|4376756

<400> 58

Met Ala Ser Gly Ile Gly Gly Ser Ser Gly Leu Gly Lys Ile Pro Pro
1 5 10 15

Lys Asp Asn Gly Asp Arg Ser Arg Ser Pro Ser Pro Lys Gly Glu Leu
20 25 30

Gly Ser His Glu Ile Ser Leu Pro Pro Gln Glu His Gly Glu Glu Gly
35 40 45

Ala Ser Gly Ser Ser His Ile His Ser Ser Ser Ser Phe Leu Pro Glu
50 55 60

Asp Gln Glu Ser Gln Ser Ser Ser Ser Ala Ala Ser Ser Pro Gly Phe
65 70 75 80

Phe Ser Arg Val Arg Ser Gly Val Asp Arg Ala Leu Lys Ser Phe Gly
85 90 95

Asn Phe Phe Ser Ala Glu Ser Thr Ser Gln Ala Arg Glu Thr Arg Gln
100 105 110

Ala Phe Val Arg Leu Ser Lys Thr Ile Thr Ala Asp Glu Arg Arg Asp
115 120 125

Val Asp Ser Ser Ser Ala Ala Ala Thr Glu Ala Arg Val Ala Glu Asp
130 135 140

Ala Ser Val Ser Gly Glu Asn Pro Ser Gln Gly Val Pro Glu Thr Ser
145 150 155 160

Ser Gly Pro Glu Pro Gln Arg Leu Phe Ser Leu Pro Ser Val Lys Lys
165 170 175

Gln Ser Gly Leu Gly Arg Leu Val Gln Thr Val Arg Asp Arg Ile Val
180 185 190

Leu Pro Ser Gly Ala Pro Pro Thr Asp Ser Glu Pro Leu Ser Leu Tyr
195 200 205

Glu Leu Asn Leu Arg Leu Ser Ser Leu Arg Gln Glu Leu Ser Asp Ile
210 215 220

Gln Ser Asn Asp Gln Leu Thr Pro Glu Glu Lys Ala Glu Ala Thr Val
225 230 235 240

Thr Ile Gln Gln Leu Ile Gln Ile Thr Glu Phe Gln Cys Gly Tyr Met
245 250 255

Glu Ala Thr Gln Ser Ser Val Ser Leu Ala Glu Ala Arg Phe Lys Gly
260 265 270

Val Glu Thr Ser Asp Glu Ile Asn Ser Leu Cys Ser Glu Leu Thr Asp
275 280 285

Pro Glu Leu Gln Glu Leu Met Ser Asp Gly Asp Ser Leu Gln Asn Leu
290 295 300

Leu Asp Glu Thr Ala Asp Asp Leu Glu Ala Ala Leu Ser His Thr Arg
305 310 315 320

Leu Ser Phe Ser Leu Asp Asp Asn Pro Thr Pro Ile Asp Asn Asn Pro
325 330 335

Thr Leu Ile Ser Gln Glu Glu Pro Ile Tyr Glu Glu Ile Gly Gly Ala
340 345 350

Ala Asp Pro Gln Arg Thr Arg Glu Asn Trp Ser Thr Arg Leu Trp Asn
355 360 365

Gln Ile Arg Glu Ala Leu Val Ser Leu Leu Gly Met Ile Leu Ser Ile
370 375 380

Leu Gly Ser Ile Leu His Arg Leu Arg Ile Ala Arg His Ala Ala Ala
385 390 395 400

Glu Ala Val Gly Arg Cys Cys Thr Cys Arg Gly Glu Glu Cys Thr Ser
405 410 415

Ser Glu Glu Asp Ser Met Ser Val Gly Ser Pro Ser Glu Ile Asp Glu
420 425 430

Thr Glu Arg Thr Gly Ser Pro His Asp Val Pro Arg Arg Asn Gly Ser
435 440 445

Pro Arg Glu Asp Ser Pro Leu Met Asn Ala Leu Val Gly Trp Ala His
450 455 460

Lys His Gly Ala Lys Thr Lys Glu Ser Ser Glu Ser Ser Thr Pro Glu
465 470 475 480

Ile Ser Ile Ser Ala Pro Ile Val Arg Gly Trp Ser Gln Asp Ser Ser
485 490 495

Val Ser Phe Ile Val Met Glu Asp Asp His Ile Phe Tyr Asp Val Pro
500 505 510

Arg Arg Lys Asp Gly Ile Tyr Asp Val Pro Ser Ser Pro Arg Trp Ser
515 520 525

Pro Ala Arg Glu Leu Glu Glu Asp Val Phe Gly Asp Tyr Glu Val Pro
530 535 540

Ile Thr Ser Ala Glu Pro Ser Lys Asp Lys Asn Ile Tyr Met Thr Pro
545 550 555 560

Arg Leu Ala Thr Pro Ala Ile Tyr Asp Leu Pro Ser Arg Pro Gly Ser
565 570 575

Ser Gly Ser Ser Arg Ser Pro Ser Ser Asp Arg Val Arg Ser Ser Ser
580 585 590

Pro Asn Arg Arg Gly Val Pro Leu Pro Pro Val Pro Ser Pro Ala Met
595 600 605

Ser Glu Glu Gly Ser Ile Tyr Glu Asp Met Ser Gly Ala Ser Gly Ala
610 615 620

Gly Glu Ser Asp Tyr Glu Asp Met Ser Arg Ser Pro Ser Pro Arg Gly
625 630 635 640

Asp Leu Asp Glu Pro Ile Tyr Ala Asn Thr Pro Glu Asp Asn Pro Phe
645 650 655

Thr Gln Arg Asn Ile Asp Arg Ile Leu Gln Glu Arg Ser Gly Gly Ala
660 665 670

Ser Ala Ser Pro Val Glu Pro Ile Tyr Asp Glu Ile Pro Trp Ile His
675 680 685

Gly Arg Pro Pro Ala Thr Leu Pro Arg Pro Glu Asn Thr Leu Thr Asn
690 695 700

Val Ser Leu Arg Val Ser Pro Gly Phe Gly Pro Glu Val Arg Ala Ala
705 710 715 720

Leu Leu Ser Glu Ser Val Ser Ala Val Met Val Glu Ala Glu Ser Ile
725 730 735

Val Pro Pro Thr Glu Pro Gly Asp Gly Glu Ser Glu Tyr Leu Glu Pro
740 745 750

Leu Gly Gly Leu Val Ala Thr Thr Lys Ile Leu Leu Gln Lys Gly Trp
755 760 765

Pro Arg Gly Glu Ser Asn Ala
770 775

<210> 59
<211> 104
<212> PRT
<213> C. trachomatis

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|3328515

<400> 59

Met Gly Asp Val Met Ile Gln Ser Val Lys Thr Glu Ser Gly Leu Val
1 5 10 15

Glu Gly His Arg Gly Ile Cys Asp Ser Leu Gly Arg Val Val Gly Ala
20 25 30

Leu Ala Lys Val Ala Lys Leu Val Val Ala Leu Ala Ala Leu Val Leu
 35 40 45

Asn Gly Ala Leu Cys Val Leu Ser Leu Val Ala Leu Cys Val Gly Ala
 50 55 60

Thr Pro Val Gly Pro Leu Ala Val Leu Val Ala Thr Thr Leu Ala Ser
 65 70 75 80

Phe Leu Cys Ala Ala Cys Val Leu Phe Ile Ala Ala Lys Asp Arg Gly
 85 90 95

Trp Ile Ala Ser Thr Asn Lys Cys
 100

<210> 60
 <211> 439
 <212> PRT
 <213> C. trachomatis

<220>
 <221> misc_feature
 <223> hypothetical protein

<220>
 <221> misc_feature
 <223> gi|3329021

<400> 60

Met Thr Thr Gly Val Arg Gly Asp Asn Ala Pro Asp Pro Ser Leu Leu
 1 5 10 15

Ala Gln Leu Thr Gln Asn Ala Asn Ser Ala Ser Ala Ala Ser Thr Gly
 20 25 30

Lys Asn Gly Gln Val Ala Gly Ala Lys Gln Glu Asn Val Asp Ala Ser
 35 40 45

Phe Glu Asp Leu Leu Gln Asp Ala Gln Gly Thr Gly Gly Ser Lys Lys
 50 55 60

Ala Thr Ala Asn Gln Thr Ser Lys Ser Gly Lys Ser Glu Lys Ala Gln
 65 70 75 80

Ala Ser Ser Gly Thr Ser Thr Thr Thr Ser Val Ala Gln Ala Ser Gln
 85 90 95

Thr	Ala	Thr	Ala	Gln	Ala	Val	His	Gly	Ala	Arg	Asp	Ser	Gly	Phe	Asn	
			100					105					110			
Ser	Asp	Gly	Ser	Ala	Thr	Leu	Pro	Ser	Pro	Thr	Gly	Thr	Glu	Val	Asn	
		115					120					125				
Gly	Val	Val	Leu	Arg	Lys	Gly	Met	Gly	Thr	Leu	Ala	Leu	Met	Gly	Leu	
	130					135					140					
Ile	Met	Thr	Leu	Leu	Ala	Gln	Ala	Ser	Ala	Lys	Ser	Trp	Ser	Ser	Ser	
145					150					155					160	
Phe	Gln	Gln	Gln	Asn	Gln	Ala	Ile	Gln	Asn	Gln	Val	Ala	Met	Ala	Pro	
				165					170					175		
Glu	Ile	Gly	Asn	Ala	Ile	Arg	Thr	Gln	Ala	Asn	His	Gln	Ala	Gln	Ala	
			180					185					190			
Thr	Glu	Leu	Gln	Ala	Gln	Gln	Ser	Leu	Ile	Ser	Gly	Ile	Thr	Asn	Ile	
		195					200					205				
Val	Gly	Phe	Ala	Val	Ser	Val	Gly	Gly	Gly	Ile	Leu	Ser	Ala	Ser	Lys	
	210					215					220					
Ser	Leu	Gly	Gly	Leu	Lys	Ser	Ala	Ala	Phe	Thr	Asn	Glu	Thr	Ala	Ser	
225					230					235					240	
Ala	Thr	Thr	Ser	Ala	Thr	Ser	Ser	Leu	Ala	Lys	Thr	Ala	Thr	Ser	Ala	
				245					250					255		
Leu	Asp	Asp	Val	Ala	Gly	Thr	Ala	Thr	Ala	Val	Gly	Ala	Lys	Ala	Thr	
			260					265					270			
Ser	Gly	Ala	Ala	Ser	Ala	Ala	Ser	Ser	Ala	Ala	Thr	Lys	Leu	Thr	Gln	
		275					280					285				
Asn	Met	Ala	Glu	Ser	Ala	Ser	Lys	Thr	Leu	Ser	Gln	Thr	Ala	Ser	Lys	
	290					295					300					
Ser	Ala	Gly	Gly	Leu	Phe	Gly	Gln	Ala	Leu	Asn	Thr	Pro	Ser	Trp	Ser	
305					310					315					320	
Glu	Lys	Val	Ser	Arg	Gly	Met	Asn	Val	Val	Lys	Thr	Gln	Gly	Thr	Arg	
				325					330					335		

Ala Ala Lys Phe Ala Gly Arg Ala Leu Ser Ser Ala Met Asn Ile Ser
 340 345 350

Gln Met Val His Gly Leu Thr Ala Gly Ile Asp Gly Ile Val Gly Gly
 355 360 365

Val Ile Gly Ala Gln Val Ala Gln Glu Gln Arg Met Ala Gly Met Ala
 370 375 380

Glu Ala Arg Ala Glu Glu Leu Lys Ser Leu Asn Ser Val Gln Ala Gln
 385 390 395 400

Tyr Ala Ser Gln Ala Gln Gln Leu Gln Glu Gln Ser Gln Gln Ser Phe
 405 410 415

Asn Ser Ala Leu Gln Thr Leu Gln Ser Ile Ser Asp Ser Ala Leu Gln
 420 425 430

Thr Thr Ala Ser Met Phe Asn
 435

<210> 61
 <211> 168
 <212> PRT
 <213> C. trachomatis

<220>
 <221> misc_feature
 <223> hypothetical protein

<220>
 <221> misc_feature
 <223> gi|3329121

<400> 61

Met Val Arg Tyr Pro Leu Glu Pro Val Leu Ser Ile Lys Lys Asp Arg
 1 5 10 15

Val Asp Arg Ala Glu Lys Val Val Lys Glu Lys Arg Arg Leu Leu Glu
 20 25 30

Leu Glu Gln Glu Lys Leu Arg Glu Arg Glu Ser Glu Arg Asp Lys Val
 35 40 45

Lys Asn His Tyr Met Gln Lys Ile Arg Gln Leu Arg Glu Gln Leu Asp
 50 55 60

Asp Gly Thr Thr Ser Asp Ala Ile Leu Lys Met Lys Ala Tyr Ile Lys
65 70 75 80

Val Val Ala Ile Gln Leu Ser Glu Glu Glu Glu Lys Val Asn Lys Gln
85 90 95

Lys Glu Asn Val Leu Ala Ala Ser Lys Glu Leu Glu Arg Ala Glu Val
100 105 110

Glu Leu Thr Lys Arg Arg Lys Glu Glu Glu Lys Thr Arg Leu His Lys
115 120 125

Glu Glu Trp Met Lys Glu Ala Leu Lys Glu Glu Ala Arg Gln Glu Glu
130 135 140

Lys Glu Gln Asp Glu Met Gly Gln Leu Leu His Gln Leu His Lys Gln
145 150 155 160

Lys Gln Arg Glu Ser Gly Glu Asn
165

<210> 62
<211> 819
<212> PRT
<213> H. influenzae

<220>
<221> misc_feature
<223> conserved hypothetical protein

<220>
<221> misc_feature
<223> gi|1574537

<400> 62

Met Ala Asp Val Leu Ser Arg Phe Asn Ser Gly Lys Leu Trp Asp Phe
1 5 10 15

Lys Gly Gly Ile His Pro Pro Glu Met Lys Ser Gln Ser Asn Ser Gln
20 25 30

Pro Leu Arg His Leu Pro Leu Gly Thr Asp Phe Tyr Ile Pro Leu Lys
35 40 45

Gln His Leu Gly Thr Thr Gly Asn Leu Leu Ile Lys Glu Gly Asp Tyr
50 55 60

Val Leu Lys Gly Gln Ala Leu Thr Lys Gly Asp Gly Leu Arg Met Leu
65 70 75 80

Pro Val His Ala Pro Thr Ser Gly Thr Ile Lys Ser Ile Lys Pro Tyr
85 90 95

Val Ala Thr His Pro Ser Gly Leu Asp Glu Pro Thr Ile His Leu Gln
100 105 110

Ala Asp Gly Leu Asp Gln Trp Ile Glu Arg Asn Pro Ile Asp Asp Phe
115 120 125

Ser Thr Leu Ser Ser Glu Gln Leu Ile His Lys Ile Tyr Gln Ala Gly
130 135 140

Ile Ala Gly Leu Gly Gly Ala Val Phe Pro Thr Ala Ala Lys Ile Gln
145 150 155 160

Ser Ala Glu Gln Lys Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys
165 170 175

Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met Arg Glu Arg Ala Asp
180 185 190

Glu Ile Ile Lys Gly Ile Arg Ile Leu Arg Tyr Ile Leu His Pro Glu
195 200 205

Lys Val Val Ile Ala Ile Glu Asp Asn Lys Pro Glu Ala Ile Ser Ala
210 215 220

Ile Arg Asn Ala Leu Gln Gly Ala Asn Asp Ile Ser Ile Arg Val Ile
225 230 235 240

Pro Thr Lys Tyr Pro Ser Gly Ala Thr Lys Gln Leu Ile Tyr Leu Leu
245 250 255

Thr Gly Ile Glu Val Pro Ser Gly Glu Arg Ser Ser Ser Ile Gly Val
260 265 270

Leu Met Gln Asn Val Gly Thr Met Phe Ala Ile Lys Arg Ala Ile Ile
275 280 285

Asn Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asn Lys
290 295 300

Ile Ala Glu Lys Gly Asn Tyr Trp Val Arg Leu Gly Thr Pro Ile Ser
 305 310 315 320

Gln Ile Leu Ser Asp Ala Gly Tyr Gln Phe Asp Lys His Phe Pro Ile
 325 330 335

Phe Ala Gly Gly Pro Met Met Gly Leu Glu Leu Pro Asn Leu Asn Ala
 340 345 350

Pro Val Thr Lys Leu Val Asn Cys Leu Leu Ala Pro Asp Tyr Leu Glu
 355 360 365

Tyr Ala Glu Pro Glu Ala Glu Gln Ala Cys Ile Arg Cys Ser Ser Cys
 370 375 380

Ser Asp Ala Cys Pro Val Asn Leu Met Pro Gln Gln Leu Tyr Trp Phe
 385 390 395 400

Ala Arg Ser Glu Asp His Lys Lys Ser Glu Glu Tyr Ala Leu Lys Asp
 405 410 415

Cys Ile Glu Cys Gly Ile Cys Ala Tyr Val Cys Pro Ser His Ile Pro
 420 425 430

Leu Ile Gln Tyr Phe Arg Gln Glu Lys Ala Lys Ile Trp Gln Ile Lys
 435 440 445

Glu Lys Gln Lys Lys Ser Asp Glu Ala Lys Ile Arg Phe Glu Ala Lys
 450 455 460

Gln Ala Arg Met Glu Arg Glu Glu Gln Glu Arg Lys Ala Arg Ser Gln
 465 470 475 480

Arg Ala Ala Gln Ala Arg Arg Glu Glu Leu Ala Gln Thr Lys Gly Glu
 485 490 495

Asp Pro Val Lys Ala Ala Leu Glu Arg Leu Lys Ala Lys Lys Ala Asn
 500 505 510

Glu Thr Glu Ser Thr Gln Ile Lys Thr Leu Thr Ser Glu Lys Gly Glu
 515 520 525

Val Leu Pro Asp Asn Thr Asp Leu Met Ala Gln Arg Lys Ala Arg Arg
 530 535 540

Leu Ala Arg Gln Gln Ala Ala Ser Gln Val Glu Asn Gln Glu Gln Gln
545 550 555 560

Thr Gln Pro Thr Asn Ala Lys Lys Ala Ala Val Ala Ala Ala Leu Ala
565 570 575

Arg Ala Lys Ala Lys Lys Leu Ala Gln Ala Asn Ser Thr Ser Glu Ala
580 585 590

Ile Ser Asn Ser Gln Thr Ala Glu Asn Gln Val Glu Lys Thr Lys Ser
595 600 605

Ala Val Glu Lys Thr Gln Glu Asn Ser Thr Ala Leu Asp Pro Lys Lys
610 615 620

Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys Lys Leu Ala
625 630 635 640

Gln Thr Asn Ser Thr Ser Glu Ala Ile Ser Asn Ser Gln Thr Ala Glu
645 650 655

Asn Glu Val Glu Lys Thr Lys Ser Ala Val Glu Lys Thr Glu Glu Asn
660 665 670

Ser Thr Ala Leu Asp Ala Lys Lys Ala Ala Ile Ala Ala Ala Ile Ala
675 680 685

Arg Ala Lys Ala Lys Lys Leu Ala Gln Ala Asn Ser Ala Ser Glu Ala
690 695 700

Ile Ser Asn Ser Gln Thr Ala Glu Asn Glu Val Glu Lys Thr Lys Ser
705 710 715 720

Ala Val Glu Lys Thr Gln Gln Asn Ser Thr Ala Leu Asp Pro Lys Lys
725 730 735

Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys Lys Leu Ala
740 745 750

Gln Ala Asn Ser Thr Ser Glu Ala Ile Ser Asn Ser Gln Thr Ala Glu
755 760 765

Asn Glu Val Glu Lys Thr Lys Ser Ala Val Glu Lys Thr Gln Glu Asn
770 775 780

Ser Thr Ala Leu Asp Pro Lys Lys Ala Ala Val Ala Ala Ala Ile Ala
785 790 795 800

Arg Ala Lys Ala Lys Lys Leu Ala Lys Thr Gln Ala Thr Leu Glu Asn
805 810 815

Asn Gln Glu

<210> 63
<211> 52
<212> PRT
<213> H. influenzae

<220>
<221> misc_feature
<223> predicted coding region HI1562

<220>
<221> misc_feature
<223> gi|1574414

<400> 63

Met Leu Ser Lys Asp Pro Lys Val Leu Ile Lys Leu Gly Glu Leu Glu
1 5 10 15

Lys Asp Lys Ser Lys Ala Lys Lys Tyr Phe Gly Asp Ala Cys Asp Leu
20 25 30

Arg Ser Gln Glu Gly Cys Asp Lys Tyr Arg Glu Leu Asn Gln Lys Gln
35 40 45

Asp Thr Asn Lys
50

<210> 64
<211> 150
<212> PRT
<213> H. influenzae

<220>
<221> misc_feature
<223> conserved hypothetical protein

<220>
<221> misc_feature
<223> gi|1574625

<400> 64

Met Thr Leu Gln Leu Asn Thr Ile Ala Leu Leu Leu Val Ile Leu Leu
1 5 10 15

Ile Leu Gly Val Leu Ser Asn Asn Ser Thr Ile Thr Ile Ser Ala Ala
20 25 30

Val Leu Leu Ile Met Gln Gln Thr Phe Leu Ser Ser His Ile Pro Leu
35 40 45

Leu Glu Lys Tyr Gly Val Lys Ile Gly Ile Ile Ile Leu Thr Ile Gly
50 55 60

Val Leu Ser Pro Leu Val Ser Gly Lys Ile Gln Leu Pro Asp Leu Ser
65 70 75 80

Gly Phe Leu Ser Trp Lys Met Ala Leu Ser Ile Ser Val Gly Val Leu
85 90 95

Val Ala Trp Leu Ala Gly Lys Gly Val Pro Leu Met Gly Glu Gln Pro
100 105 110

Ile Leu Val Thr Gly Leu Leu Ile Gly Thr Ile Ile Gly Val Ala Phe
115 120 125

Leu Gly Gly Ile Pro Val Gly Pro Leu Ile Ala Ala Gly Ile Leu Ala
130 135 140

Leu Leu Leu Gly Lys Ile
145 150

<210> 65

<211> 129

<212> PRT

<213> H. influenzae

<220>

<221> misc_feature

<223> predicted coding region HI1339

<220>

<221> misc_feature

<223> gi|1574799

<400> 65

Met Glu Lys Ile Met Lys Lys Leu Thr Leu Ala Leu Val Leu Gly Ser
1 5 10 15

Ala Leu Val Val Thr Gly Cys Phe Asp Lys Gln Glu Ala Lys Gln Lys
 20 25 30

Val Glu Asp Thr Lys Gln Thr Val Ala Ser Val Ala Ser Glu Thr Lys
 35 40 45

Asp Ala Ala Ala Asn Thr Met Thr Glu Val Lys Glu Lys Ala Gln Gln
 50 55 60

Leu Ser Thr Asp Val Lys Asn Lys Val Ala Glu Lys Val Glu Asp Ala
 65 70 75 80

Lys Glu Val Ile Lys Ser Ala Thr Glu Ala Ala Ser Glu Lys Val Gly
 85 90 95

Glu Met Lys Glu Ala Ala Ser Glu Lys Ala Ser Glu Met Lys Glu Ala
 100 105 110

Val Ser Glu Lys Ala Thr Gln Ala Val Asp Ala Val Lys Glu Ala Thr
 115 120 125

Lys

<210> 66
 <211> 136
 <212> PRT
 <213> H. influenzae

<220>
 <221> misc_feature
 <223> predicted coding region HI1462.1

<220>
 <221> misc_feature
 <223> gi|3212225

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> "Xaa" may be any amino acid

<400> 66

Met Xaa Gln Ser Asn Tyr Ser Met Glu Lys Ile Met Lys Lys Leu Thr
 1 5 10 15

Leu Ala Leu Val Leu Gly Ser Ala Leu Val Val Thr Gly Cys Phe Asp
 97/176

20

25

30

Lys Gln Glu Ala Lys Gln Lys Val Glu Asp Thr Lys Gln Thr Val Ala
 35 40 45

Ser Val Ala Ser Glu Thr Lys Asp Ala Ala Ala Asn Thr Met Thr Glu
 50 55 60

Val Lys Glu Lys Ala Gln Gln Leu Ser Thr Asp Val Lys Asn Lys Val
 65 70 75 80

Ala Glu Lys Val Glu Asp Ala Lys Glu Val Ile Lys Ser Ala Thr Glu
 85 90 95

Ala Ala Ser Glu Lys Val Gly Glu Met Lys Glu Ala Ala Ser Glu Lys
 100 105 110

Ala Ser Glu Met Lys Glu Ala Val Ser Glu Lys Ala Thr Gln Ala Val
 115 120 125

Asp Ala Val Lys Glu Ala Thr Lys
 130 135

<210> 67
 <211> 113
 <212> PRT
 <213> H. influenzae

<220>
 <221> misc_feature
 <223> conserved hypothetical protein

<220>
 <221> misc_feature
 <223> gi|1574607

<400> 67

Met Phe Thr Asp Trp Lys Glu His Thr Ser His Val Lys Lys Ser Phe
 1 5 10 15

Gly Glu Leu Gly Lys Gln Tyr Pro Lys Met Leu Gln Ala Tyr Gln Ala
 20 25 30

Leu Gly Ala Ala Ala Ala Glu Gly Asn Val Leu Asp Ala Lys Thr Arg
 35 40 45

Glu Leu Ile Ala Leu Ala Val Ala Val Thr Thr Arg Cys Glu Ser Cys
 98/176

50

55

60

Ile Ser Ala His Ala Glu Glu Ala Val Lys Ala Gly Ala Ser Glu Ala
65 70 75 80

Glu Val Ala Ala Ala Leu Ala Thr Ala Ile Ala Leu Asn Ala Gly Ala
85 90 95

Ala Tyr Thr Tyr Ser Leu Arg Ala Leu Glu Ala Tyr Ser Val Gln Lys
100 105 110

Ala

<210> 68
<211> 33
<212> PRT
<213> H. pylori

<220>
<221> misc_feature
<223> predicted coding region HP0131

<220>
<221> misc_feature
<223> gi|2313229

<400> 68

Met Pro Tyr Pro Phe Met Ser Phe Lys Gln Thr Phe Tyr Tyr Lys Met
1 5 10 15

Glu Ser Lys Thr Met Lys Glu Arg Phe Lys Thr Leu Phe Phe Lys Ile
20 25 30

Phe

<210> 69
<211> 12
<212> PRT
<213> H. pylori

<220>
<221> misc_feature
<223> predicted coding region HP0429

<220>
<221> misc_feature
<223> gi|2313552

<400> 69

Met Asn Glu Asn Gly Lys Lys Glu Ala Leu Gln Leu
1 5 10

<210> 70

<211> 26

<212> PRT

<213> H. pylori

<220>

<221> misc_feature

<223> predicted coding region HP0560

<220>

<221> misc_feature

<223> gi|2313684

<400> 70

Met Gly Ile Ile Tyr Leu Ile Leu Phe Leu Ile Val Ile Tyr Leu Leu
1 5 10 15

Tyr Arg Ile Leu Asp Val Leu Glu Gln Lys
20 25

<210> 71

<211> 48

<212> PRT

<213> H. pylori

<220>

<221> misc_feature

<223> predicted coding region HP0756

<220>

<221> misc_feature

<223> gi|2313894

<400> 71

Met Lys Asp Tyr Glu Asp Glu Leu Glu Asp Phe Glu Glu Glu Glu Leu
1 5 10 15

Glu Gly Phe Glu Glu Glu Asp Glu Glu Tyr Gly Asp Tyr Lys Asn Val
20 25 30

Tyr Asp Asp Asp Asp Tyr Glu Asp Tyr Asn Ser Asp Tyr Glu Glu Glu
35 40 45

<210> 72

<211> 23
<212> PRT
<213> H. pylori

<220>
<221> misc_feature
<223> predicted coding region HP1500

<220>
<221> misc_feature
<223> gi|2314686

<400> 72

Met Cys Ser Asn Ser Ser Ser Leu Lys Ile Tyr Ser Leu Glu Ser Asn
1 5 10 15

Phe Ser Phe Asn Ser Leu Phe
20

<210> 73
<211> 1805
<212> PRT
<213> M. genitalium

<220>
<221> misc_feature
<223> gi|1045905

<400> 73

Met Lys Pro Phe Asp Lys Lys Pro Ser Leu Gln Pro Ile Tyr Asp Ile
1 5 10 15

Gly Phe Asp Asp Gly Tyr Leu Gln Ser Glu Tyr Glu Lys Asn Arg Ser
20 25 30

Lys Thr Asp Val Asp Lys Ile Glu Asn Gln Leu Leu Lys Glu Ile Lys
35 40 45

Ser Leu Glu Asp Glu Leu Lys Asn Leu Lys Gly Leu Lys Asn Gln Ala
50 55 60

Glu Asp Asn Pro Glu Leu Asp Lys Lys Ile Asn His Leu Glu Val Asp
65 70 75 80

Leu Asn Arg Leu Val Asn Glu Tyr Lys Asn Phe Gln Phe Gln Lys Asn
85 90 95

His Met Val Asp Lys Val Ser Glu Leu Asp Asn Leu Thr Arg Phe Tyr
101/176

100						105						110					
Lys	Asn	Glu	Leu	Thr	Arg	Leu	Gln	Gln	Glu	Asn	Ala	Asp	Phe	Leu	Asn		
		115					120						125				
Ser	Lys	Tyr	Ala	Asn	Leu	Ala	Asn	Phe	Gln	Ala	Asn	Tyr	His	Asn	Lys		
	130						135						140				
Leu	Asn	Asp	Phe	His	Arg	Leu	Ile	Glu	Asn	Gln	Asn	Gln	Thr	Ile	Asn		
145					150					155					160		
Arg	Leu	Asn	Gln	Lys	Ile	Asn	Gly	Asn	Gln	Asn	Leu	Ile	Asp	Asn	Asn		
				165					170					175			
Val	Ala	Leu	Leu	Gln	Asn	Pro	Asn	Ile	Thr	Val	Glu	Lys	Lys	Asn	Tyr		
			180					185					190				
Leu	Leu	Asn	Val	Ile	Asp	Gln	Leu	Tyr	Asn	Glu	Leu	Asp	Gln	Leu	Glu		
		195					200						205				
Asn	Gln	Lys	Arg	Leu	Leu	Ser	Ile	Glu	Tyr	Glu	Asn	Thr	Tyr	Arg	Glu		
	210						215				220						
Leu	Val	Ser	Ala	Asp	Asn	Glu	Leu	Gln	Asn	Val	Tyr	Glu	Asn	Ile	Asp		
225					230					235					240		
Gln	Asn	Gln	Ile	Gln	Phe	Lys	His	Gln	Tyr	Gln	Thr	Tyr	Arg	Asp	Glu		
				245					250					255			
Leu	Ser	Gln	Leu	Glu	Arg	Lys	Ile	Gln	Leu	Thr	Lys	Gln	Glu	Leu	Val		
			260					265					270				
Asp	Lys	Glu	Ser	Ala	Leu	Arg	Val	Lys	Ile	Asp	Asp	Ala	Asp	Phe	Tyr		
		275					280						285				
Ile	Asn	Ala	Arg	Leu	Ala	Glu	Leu	Asp	Asp	Val	Ala	Lys	Gln	Leu	Ser		
	290						295				300						
Phe	Gln	Asp	Gly	Ile	Thr	Lys	Gln	Asn	Ala	Gln	His	Val	Glu	Asp	Lys		
305					310					315					320		
Leu	Val	Ala	Leu	Asn	Lys	Glu	Lys	Asp	Arg	Leu	Asn	Thr	Gln	Lys	Glu		
				325					330					335			
Ala	Phe	Phe	Asn	Leu	Arg	Gln	Ser	Ala	Leu	Ile	Asp	Ile	Asn	Lys	Leu		

340										345					350				
Gln	Gln	Glu	Asn	Glu	Leu	Phe	Ala	Lys	His	Leu	Glu	His	Gln	Gln	Asn				
		355					360					365							
Glu	Phe	Glu	Gln	Lys	Gln	Ser	Asp	Ser	Leu	Leu	Lys	Leu	Glu	Thr	Glu				
	370					375					380								
Tyr	Lys	Ala	Leu	Gln	His	Lys	Ile	Asn	Glu	Phe	Lys	Asn	Glu	Ser	Ala				
385					390					395					400				
Thr	Lys	Ser	Glu	Glu	Leu	Leu	Asn	Gln	Glu	Arg	Glu	Leu	Phe	Glu	Lys				
				405					410					415					
Arg	Arg	Glu	Ile	Asp	Thr	Leu	Leu	Thr	Gln	Ala	Ser	Leu	Glu	Tyr	Glu				
			420					425					430						
His	Gln	Arg	Glu	Ser	Ser	Gln	Leu	Leu	Lys	Asp	Lys	Gln	Asn	Glu	Val				
		435					440					445							
Lys	Gln	His	Phe	Gln	Asn	Leu	Glu	Tyr	Ala	Lys	Lys	Glu	Leu	Asp	Lys				
	450					455					460								
Glu	Arg	Asn	Leu	Leu	Asp	Gln	Gln	Lys	Lys	Val	Asp	Ser	Glu	Ala	Ile				
465					470					475					480				
Phe	Gln	Leu	Lys	Glu	Lys	Val	Ala	Gln	Glu	Arg	Lys	Glu	Leu	Glu	Glu				
			485						490					495					
Leu	Tyr	Leu	Val	Lys	Lys	Gln	Lys	Gln	Asp	Gln	Lys	Glu	Asn	Glu	Leu				
			500					505					510						
Leu	Phe	Phe	Glu	Lys	Gln	Leu	Lys	Gln	His	Gln	Ala	Asp	Phe	Glu	Asn				
		515					520					525							
Glu	Leu	Glu	Ala	Lys	Gln	Gln	Glu	Leu	Phe	Glu	Ala	Lys	His	Ala	Leu				
	530					535					540								
Glu	Arg	Ser	Phe	Ile	Lys	Leu	Glu	Asp	Lys	Glu	Lys	Asp	Leu	Asn	Thr				
545					550					555					560				
Lys	Ala	Gln	Gln	Ile	Ala	Asn	Glu	Phe	Ser	Gln	Leu	Lys	Thr	Asp	Lys				
				565				570						575					
Ser	Lys	Ser	Ala	Asp	Phe	Glu	Leu	Met	Leu	Gln	Asn	Glu	Tyr	Glu	Asn				

580							585							590						
Leu	Gln	Gln	Glu	Lys	Gln	Lys	Leu	Phe	Gln	Glu	Arg	Thr	Tyr	Phe	Glu					
		595					600					605								
Arg	Asn	Ala	Ala	Val	Leu	Ser	Asn	Arg	Leu	Gln	Gln	Lys	Arg	Glu	Glu					
	610					615					620									
Leu	Leu	Gln	Gln	Lys	Glu	Thr	Leu	Asp	Gln	Leu	Thr	Lys	Ser	Phe	Glu					
625					630					635					640					
Gln	Glu	Arg	Leu	Ile	Asn	Gln	Arg	Glu	His	Lys	Glu	Leu	Val	Ala	Ser					
			645						650					655						
Val	Glu	Lys	Gln	Lys	Glu	Ile	Leu	Gly	Lys	Lys	Leu	Gln	Asp	Phe	Ser					
			660					665					670							
Gln	Thr	Ser	Leu	Asn	Ala	Ser	Lys	Asn	Leu	Ala	Glu	Arg	Glu	Met	Ala					
		675					680					685								
Ile	Lys	Phe	Lys	Glu	Lys	Glu	Ile	Glu	Ala	Thr	Glu	Lys	Gln	Leu	Leu					
	690					695					700									
Asn	Asp	Val	Asn	Asn	Ala	Glu	Val	Ile	Gln	Ala	Asp	Leu	Ala	Gln	Leu					
705					710					715					720					
Asn	Gln	Ser	Leu	Asn	Gln	Glu	Arg	Ser	Glu	Leu	Gln	Asn	Ala	Lys	Gln					
				725					730					735						
Arg	Ile	Ala	Asp	Phe	His	Asn	Asp	Ser	Leu	Lys	Lys	Leu	Asn	Glu	Tyr					
		740					745						750							
Glu	Leu	Ser	Leu	Gln	Lys	Arg	Leu	Gln	Glu	Leu	Gln	Thr	Leu	Glu	Ala					
		755					760					765								
Asn	Gln	Lys	Gln	His	Ser	Tyr	Gln	Asn	Gln	Ala	Tyr	Phe	Glu	Gly	Glu					
		770				775					780									
Leu	Asp	Lys	Leu	Asn	Arg	Glu	Lys	Gln	Ala	Phe	Leu	Asn	Leu	Arg	Lys					
785					790					795					800					
Lys	Gln	Thr	Met	Glu	Val	Asp	Ala	Ile	Lys	Gln	Arg	Leu	Ser	Asp	Lys					
				805					810					815						
His	Gln	Ala	Leu	Asn	Met	Gln	Gln	Ala	Glu	Leu	Asp	Arg	Lys	Thr	His					

820

825

830

Glu Leu Asn Asn Ala Phe Leu Asn His Asp Ala Asp Gln Lys Ser Leu
835 840 845

Gln Asp Gln Leu Ala Thr Val Lys Glu Thr Gln Lys Leu Ile Asp Leu
850 855 860

Glu Arg Ser Ala Leu Leu Glu Lys Gln Arg Glu Phe Ala Glu Asn Val
865 870 875 880

Ala Gly Phe Lys Arg His Trp Ser Asn Lys Thr Ser Gln Leu Gln Lys
885 890 895

Ile Tyr Glu Leu Thr Lys Lys Gln Glu Ser Glu Gln Thr Gln Lys Glu
900 905 910

Thr Glu Leu Lys Ile Ala Phe Ser Asp Leu Gln Lys Asp Tyr Gln Val
915 920 925

Phe Glu Leu Gln Lys Asp Gln Glu Phe Arg Gln Ile Glu Ala Lys Gln
930 935 940

Arg Glu Leu Asp Lys Leu Ala Glu Lys Asn Asn Gln Val Lys Leu Glu
945 950 955 960

Leu Asp Asn Arg Phe Gln Ala Leu Gln Asn Gln Lys Gln Asp Thr Val
965 970 975

Gln Ala Gln Leu Glu Leu Glu Arg Glu Gln His Gln Leu Asn Leu Glu
980 985 990

Gln Thr Ala Phe Asn Gln Ala Asn Glu Ser Leu Leu Lys Gln Arg Glu
995 1000 1005

Gln Leu Thr Lys Lys Ile Gln Ala Phe His Tyr Glu Leu Lys Lys
1010 1015 1020

Arg Asn Gln Phe Leu Ala Leu Lys Gly Lys Arg Leu Phe Ala Lys
1025 1030 1035

Glu Gln Asp Gln Gln Arg Lys Asp Gln Glu Ile Asn Trp Arg Phe
1040 1045 1050

Lys Gln Phe Glu Lys Glu Tyr Thr Asp Phe Asp Glu Ala Lys Lys
105/176

1055	1060	1065
Arg Glu Leu Glu Glu Leu Glu 1070	Lys Ile Arg Arg 1075	Ser Leu Ser Gln 1080
Ser Asn Val Glu Leu Glu Arg 1085	Lys Arg Glu Lys 1090	Leu Ala Thr Asp 1095
Phe Thr Asn Leu Asn Lys Val 1100	Gln His Asn Thr 1105	Gln Ile Asn Arg 1110
Asp Gln Leu Asn Ser Gln Ile 1115	Arg Gln Phe Leu 1120	Leu Glu Arg Lys 1125
Asn Phe Gln Arg Phe Ser Asn 1130	Glu Ala Asn Ala 1135	Lys Lys Ala Phe 1140
Leu Ile Lys Arg Leu Arg Ser 1145	Phe Ala Ser Asn 1150	Leu Lys Leu Gln 1155
Lys Glu Ala Leu Ala Ile Gln 1160	Lys Leu Glu Phe 1165	Asp Lys Arg Asp 1170
Glu Gln Gln Lys Lys Glu Leu 1175	Gln Gln Ala Thr 1180	Leu Gln Leu Glu 1185
Gln Phe Lys Phe Glu Lys Gln 1190	Asn Phe Asp Ile 1195	Glu Lys Gln Arg 1200
Gln Leu Val Ala Ile Lys Thr 1205	Gln Cys Glu Lys 1210	Leu Ser Asp Glu 1215
Lys Lys Ala Leu Asn Gln Lys 1220	Leu Val Glu Leu 1225	Lys Asn Leu Ser 1230
Gln Thr Tyr Leu Ala Asn Lys 1235	Asn Lys Ala Glu 1240	Tyr Ser Gln Gln 1245
Gln Leu Gln Gln Lys Tyr Thr 1250	Asn Leu Leu Asp 1255	Leu Lys Glu Asn 1260
Leu Glu Arg Thr Lys Asp Gln 1265	Leu Asp Lys Lys 1270	His Arg Ser Ile 1275
Phe Ala Arg Leu Thr Lys Phe	Ala Asn Asp Leu Arg	Phe Glu Lys

1280	1285	1290
Lys Gln Leu Leu Lys Ala Gln 1295	Arg Ile Val Asp 1300	Asp Lys Asn Arg 1305
Leu Leu Lys Glu Asn Glu Arg 1310	Asn Leu His Phe 1315	Leu Ser Asn Glu 1320
Thr Glu Arg Lys Arg Ala Val 1325	Leu Glu Asp Gln 1330	Ile Ser Tyr Phe 1335
Glu Lys Gln Arg Lys Gln Ala 1340	Thr Asp Ala Ile 1345	Leu Ala Ser His 1350
Lys Glu Val Lys Lys Lys Glu 1355	Gly Glu Leu Gln 1360	Lys Leu Leu Val 1365
Glu Leu Glu Thr Arg Lys Thr 1370	Lys Leu Asn Asn 1375	Asp Phe Ala Lys 1380
Phe Ser Arg Gln Arg Glu Glu 1385	Phe Glu Asn Gln 1390	Arg Leu Lys Leu 1395
Leu Glu Leu Gln Lys Thr Leu 1400	Gln Thr Gln Thr 1405	Asn Ser Asn Asn 1410
Phe Lys Thr Lys Ala Ile Gln 1415	Glu Ile Glu Asn 1420	Ser Tyr Lys Arg 1425
Gly Met Glu Glu Leu Asn Phe 1430	Gln Lys Lys Glu 1435	Phe Asp Lys Asn 1440
Lys Ser Arg Leu Tyr Glu Tyr 1445	Phe Arg Lys Met 1450	Arg Asp Glu Ile 1455
Glu Arg Lys Glu Ser Gln Val 1460	Lys Leu Val Leu 1465	Lys Glu Thr Gln 1470
Arg Lys Ala Asn Leu Leu Glu 1475	Ala Gln Ala Asn 1480	Lys Leu Asn Ile 1485
Glu Lys Asn Thr Ile Asp Phe 1490	Lys Glu Lys Glu 1495	Leu Lys Ala Phe 1500
Lys Asp Lys Val Asp Gln Asp	Ile Asp Ser Thr Asn	Lys Gln Arg

1505		1510		1515
Lys Glu Leu Asn Glu Leu Leu Asn Glu Asn Lys Leu Leu Gln Gln	1520	1525		1530
Ser Leu Ile Glu Arg Glu Arg Ala Ile Asn Ser Lys Asp Ser Leu	1535	1540		1545
Leu Asn Lys Lys Ile Glu Thr Ile Lys Arg Gln Leu His Asp Lys	1550	1555		1560
Glu Met Arg Val Leu Arg Leu Val Asp Arg Met Lys Leu Ala Glu	1565	1570		1575
Gln Lys Tyr Gln Thr Glu Ile Asn Arg Leu Arg Thr Gln Thr Phe	1580	1585		1590
Asp Ser Glu Lys Gln Asp Ile Lys Asn Phe Phe Pro Pro Leu Phe	1595	1600		1605
Lys Ile Asn Gly Asn Asp Met Ala Phe Pro Tyr Leu Tyr Pro Trp	1610	1615		1620
Leu Tyr Pro Gln Gln Lys Gln Asp Asp Asn Thr Leu Gln Ile Arg	1625	1630		1635
Gln Leu Phe Glu Gln Gln Leu Gln Phe Met Gln Gln Arg Tyr Glu	1640	1645		1650
Asn Glu Leu Asn Glu Leu Arg Arg Gln Arg Asn Leu Leu Glu Lys	1655	1660		1665
Lys Leu Asp Gln Ile Gln Leu Glu Ser Gln Leu Asn Asn Lys Gln	1670	1675		1680
Ser Glu Phe Ser Lys Val Glu Ser Met Met Glu Lys Leu Leu Glu	1685	1690		1695
Lys Thr Glu Ser Arg Leu Asn Asp Phe Asp Gln Lys Ile Asn Tyr	1700	1705		1710
Leu Thr Lys Lys Val Asn Gln His Asn Thr Tyr Gln Pro Ser Ser	1715	1720		1725
Tyr Gln Pro Thr Pro Ser Tyr Gln Asp Ser Asp Lys Gln Gln Leu				

1730 1735 1740
 Leu Phe Arg Ile Gln Glu Leu Glu Lys Gln Asn Leu Phe Gln Gln
 1745 1750 1755
 Gln Phe Gln Pro Ala Pro Ala Val Val Gln Gln Pro Thr Ser Phe
 1760 1765 1770
 Ala Ala Pro Asn Ile Thr Lys Gln Gln Gln Ile Ala Gln Leu Asn
 1775 1780 1785
 Ala Glu Ile Asn Asn Ile Lys Arg Leu Ile Ala Gln Lys Ala Ala
 1790 1795 1800
 Ser Lys
 1805

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Met Gln Tyr Ser Ala Leu Ile Pro Leu Phe Ile Leu Leu Ile Ser Leu
 1 5 10 15

Val Leu Phe Cys Phe Ser Phe Arg Lys Asn Gln Ser Glu Asn Gln Ile
 20 25 30

Val Lys Ile Leu Phe Phe Ala Tyr Cys Ile Asp Phe Leu Ala Leu Ile
 35 40 45

Leu Ala Val Met Leu Leu Thr Phe Leu Ser His Gly Leu Leu Ser Leu
 50 55 60

Ala Ile Leu Ile Pro Val Leu Val Phe Gln
 65 70

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Met Glu Phe Leu Glu Gln Glu Gly Gln Glu Val Leu Thr Lys Glu Ile
1 5 10 15

Lys Ala Gly Phe Cys Glu Ile Thr Pro Ser Ser Ile Thr Glu Gln Thr
20 25 30

Thr Lys Pro Gln Leu Asp Glu Thr Gln Leu Val Asp Glu Tyr Val His
35 40 45

Thr Lys Glu Leu Glu Thr Thr Pro Ile Pro Ile Ser Phe Ala Thr Lys
50 55 60

Glu Val Leu Phe Glu Glu Val Phe Asn Thr Pro Ser Thr Gln Gln Val
65 70 75 80

Asp Glu Ser Val Leu Val Asn Glu Tyr Ile Glu Leu Thr Gln Gln Ile
85 90 95

Lys Asn Ala Ser Glu Gln Val Ser Ser Asn His Thr His Lys Phe Ser
100 105 110

Val Ala Thr Glu Pro Ala Ala Thr Lys Ala Val Ser Glu Thr Met Leu
115 120 125

Leu Asp Asp Tyr Val Glu Met Val Glu Gln Asp Val Gln Ala Gln Thr
130 135 140

Ala Leu Pro Gln Ala Ala Leu Asp Pro Thr Val Ser Leu Thr Phe Ser
145 150 155 160

Ser Pro Ile Asp Ser Asn Ala Ile Leu Val Tyr Pro Glu Met Lys Val
165 170 175

Pro His Val Phe Asp Thr Val Ala Pro Thr Thr Thr Val Pro Leu
110/176

180										185										190										
Asp	Gln	Thr	Gln	Leu	Leu	Asp	Glu	Leu	Val	Glu	Val	Pro	Val	Leu	Thr															
			195					200					205																	
His	Thr	Val	Thr	Pro	Ala	Pro	Leu	Gln	Pro	Lys	Ala	Ala	Pro	Thr	Asn															
		210					215					220																		
Phe	Ala	Leu	Asp	Gln	Thr	Gln	Leu	Val	Asp	Glu	Leu	Val	Thr	Val	Pro															
		225			230						235				240															
Leu	Thr	His	Thr	Leu	Val	Asn	Glu	Ser	Ala	Pro	Val	Thr	Pro	Val	Val															
				245					250						255															
Val	Thr	Ser	Pro	Ala	Ala	Glu	His	Ser	Phe	Ser	Ile	Thr	Thr	Val	Asp															
			260					265						270																
Lys	Ala	Asn	Leu	Thr	Asn	Ala	Leu	Ser	Gln	Thr	Val	Val	Ile	Lys	Pro															
		275					280						285																	
Ala	Glu	Asp	Ser	Ala	His	Gln	Ser	Ala	Val	Leu	Asp	Lys	Glu	Ile	Ala															
		290				295						300																		
Thr	Lys	Gln	Ala	Gln	Leu	Gln	Gln	Leu	Gln	Ala	Gln	Ile	Glu	Leu	Arg															
		305			310					315					320															
Gln	Ala	Gln	Leu	Glu	Thr	Pro	Pro	Val	Thr	Tyr	Met	Gly	Val	Glu	Glu															
			325						330					335																
Tyr	Lys	Leu	Leu	Pro	Val	Gln	Asp	Val	Val	Pro	Val	Gln	Pro	Thr	Val															
			340					345					350																	
Ser	Phe	Glu	Met	Thr	Leu	Leu	Gln	Glu	Gln	Leu	Asp	Lys	Ala	Leu	Lys															
		355					360					365																		
His	Asn	Ala	Ala	Leu	Gln	Ile	Gln	Leu	Glu	Glu	Gln	Leu	Ala	Lys	Pro															
		370				375						380																		
Leu	Gln	Tyr	Asp	Gln	Ser	Pro	Val	Leu	Gln	Glu	Arg	Ile	Glu	Leu	Leu															
		385			390					395					400															
Gln	Asn	Gln	Asn	Thr	Asn	Leu	Thr	Gln	Glu	Leu	Asn	Glu	Leu	Gln	Gln															
			405						410					415																
Lys	Leu	Phe	Lys	Ser	Gln	Asn	Asn	Ser	Leu	Leu	Leu	Ala	Arg	Leu	Glu															

420

425

430

Glu Glu Asn Arg Thr Leu Lys Gln His Leu Gln Asn Asn Leu Pro Glu
 435 440 445

Ala Asn Gln Leu Asn Phe Val Leu Glu Lys Gln Leu Glu Gln Leu Gln
 450 455 460

Gln Asp Lys His Ser Leu Thr Leu Gln Ile Glu Gln Tyr Lys Phe Asp
 465 470 475 480

Ser Lys Lys His Gln Glu Gln Leu Ala Leu Ile Pro Ser Leu Arg Ser
 485 490 495

Glu Ile Asn Ser Leu Glu Thr Glu Val Ile Ser Leu Lys Gln Thr Asn
 500 505 510

Gln Arg Leu Ser Leu Ile Glu Arg Glu Asn Asn Phe Leu Lys Thr Glu
 515 520 525

Ile Lys Gln Leu Arg Glu Thr Lys Leu Asn Asp Glu Asn Thr Lys Tyr
 530 535 540

Arg Asn Leu Leu Lys Gln Tyr Glu Leu Met Arg Ala Asp Ser Asp Ala
 545 550 555 560

Lys Leu Lys Glu Leu Glu His Glu Gln His Leu Ala His Gln His His
 565 570 575

Gln Glu Gln Leu Ala Gln Leu Gln Arg His Asn Glu Ala Leu Val Lys
 580 585 590

Glu Leu Asp Gln Val Lys Ala Thr Asn Phe Glu Leu Gly Leu Ala Ala
 595 600 605

Gln Gly Phe Glu Gln Gln Lys Val Val Leu Glu Gln Lys Asn Ser Ser
 610 615 620

Leu Leu Ala Ser Leu Gln Ala Ala Glu Glu Asn Val Gln Ala Leu Gly
 625 630 635 640

Ile Thr Asn Ser Glu Leu Gln Asn Gln Leu Asn Val Leu Glu Phe Thr
 645 650 655

His Lys Glu Lys Thr Ala Phe Asp Ser Lys Thr Leu Thr Leu Thr Lys
 112/176

660

665

670

Gln Gln Leu Glu Gln Thr Gln Phe Asp Leu Ser Leu Thr Gln Glu Gln
 675 680 685

Leu Ala Thr Phe Lys Gln Gln Asn Gln Ser Leu Thr Asp Lys Leu Met
 690 695 700

Ala Ser Glu Thr Gln Leu Asn His Leu Gln Gln Ser Asp Glu Asn Leu
 705 710 715 720

Thr Gln Leu Gln Thr Gln His Glu Leu Leu Gln Glu Ser Tyr Asn Lys
 725 730 735

Leu Gln Asp Glu Ala Asn His Thr Gln Gln Gln Phe His Gln Ala Gln
 740 745 750

Asn Glu Leu Asp Ala Ala His Gln Gln Leu Ala Leu Phe Lys Gln Asn
 755 760 765

Asn Glu Glu Leu Thr Asp Lys Cys Ser Asn Ile Gln Asn Glu Leu His
 770 775 780

Asp Leu Asn Arg Val Lys Thr Asn Trp Glu Asn Leu Asn Thr Glu His
 785 790 795 800

Asn Leu Leu Gln Asp Lys Tyr Ala Gln Gln Lys Glu Gln Met Gln His
 805 810 815

Glu His Ser Asn Leu Ala Gln Ile Gln Ala Glu His Glu Leu Leu Gln
 820 825 830

Glu Ser Tyr Asn Lys Val Lys Ala Glu Leu Asn Glu Ile Gln Ile Thr
 835 840 845

Asn Leu Asn Glu Ala Asn Ala Gln Tyr Gln Asp Leu Leu Ser Ala Tyr
 850 855 860

Glu Leu Leu Gln Ser Asn His Asn Lys Leu Lys Gln Glu Leu Gln Val
 865 870 875 880

Leu Asn Gln Val Asn Leu Glu Lys Gln Gln Leu Ala Gln Lys Leu His
 885 890 895

Asn Thr His Gln Ser Leu Ser Gln Thr His Ala Glu Leu Thr Gln Leu

900	905	910
Gln Ala Ala Tyr Asn Asn Leu	Gln Ala Thr Pro Pro	Val Ser Asp Glu
915	920	925
Leu Leu Glu Gln Phe Asn Gln Val	Gln Leu Glu Lys Gln Arg Leu Leu	
930	935	940
Gln Gln Asn Leu Ala Leu Val His Glu Leu	Gln Tyr Phe Asn Glu Leu	
945	950	955 960
Asn Ser Ser Gln Thr His Glu Ile Lys Thr Lys Gln Asp Glu Thr Val		
	965	970 975
Lys Glu Val Ile Ile Val Glu Lys Glu Ile Pro Val Pro Pro Glu Lys		
	980	985 990
Lys Pro Arg Leu Lys Lys Arg Asp Ile Val Ile Glu Asn Lys Glu Asp		
	995	1000 1005
Ala Leu Gly Lys Leu Ser Lys Lys Glu Arg Ile Gln Ala Tyr Ala		
1010	1015	1020
Glu Arg Leu Ala Lys Ile Asn Gly Lys Gln		
1025	1030	
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1	5	10 15
Asn Pro Asp Phe Pro Ala		
	20	
<210> 77		

<211> 103
<212> PRT
<213> M. pneumoniae

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<223> B01_orf103b Protein

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<223> gi|1673772

<400> 77

Met Ser Ser Val Phe Ser Lys Pro Asn Leu Lys Arg Pro Ser Phe Asp
1 5 10 15

Val Lys Asn Leu Thr Lys Pro Ser Arg Leu Leu Ser Ala Thr Leu Arg
20 25 30

Ser Ser Cys Ala Phe Leu Ser Ser Ala Ser Phe Phe Ala Cys Ser Leu
35 40 45

Cys Phe Phe Cys Cys Ser Ser Ile Ser Phe Cys Ser Leu Ala Ser Ser
50 55 60

Ser Ala Arg Leu Arg Tyr Ser Ser Ser His Ser Phe Phe Cys Trp Val
65 70 75 80

Leu Phe Ser Arg Ser Gly Leu Ala Tyr Ser Ser Ser Asn Leu Ser Ser
85 90 95

Lys Ser Ser Arg Leu Arg Ser
100

<210> 78
<211> 112
<212> PRT
<213> M. pneumoniae

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<223> VxpSPT7_orf112 Protein

<220>
<221> misc_feature
<223> gi|1674374

<400> 78

Met Ile Asp Arg Phe Phe Trp Ser Ile Leu Ser Phe Leu Leu Thr Asn
115/176

1 5 10 15
 Leu Val Phe Leu Phe Val Ala Phe Leu Ile Leu Ile Ile Tyr Leu Ile
 20 25 30
 Ser Glu Ile Thr Gln Gln Phe Ala Phe Ala Phe Ile Ala Thr Ile Val
 35 40 45
 Phe Ile Ile Phe Tyr Asn Ile Leu Phe Leu Ser Tyr Leu Leu Thr Met
 50 55 60
 Tyr Ile Lys Gly Leu Lys Gln Ile Glu Gln Lys Ser Arg Tyr Leu Leu
 65 70 75 80
 Leu Val Leu Asp Val Lys Ala Asp Glu Leu Leu Pro Phe Ser Phe Leu
 85 90 95
 Gly Ser Leu Arg Lys Ser His Met Leu Glu Glu Met Leu Leu Glu Gln
 100 105 110

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 <211> 147
 <212> PRT
 <213> M. pneumoniae

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 <223> B01_orf147 Protein

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 Met Pro Ser Ser Ala Phe Lys Ile Asn Leu Ser Val Ser Pro Trp Phe
 1 5 10 15
 Phe Cys Ser Thr Trp Ser Ser Leu Ile Cys Trp Pro Trp Thr Ile Thr
 20 25 30
 Thr Ser Val Ser Arg Ser Thr Leu Ser Ser Thr Thr Trp Ile Leu Trp
 35 40 45
 Thr Trp Leu Phe Asn Ser Val Ser Ile Phe Val Ser Arg Trp Ser Phe
 50 55 60
 Asp Phe Leu Tyr Ser Leu Asn Ser Leu Arg Val Thr Tyr Ser Val Phe
 116/176

80

95

110

125

140

145

<213> M. tuberculosis

<223> hypothetical protein Rv3611

<223> gi | 2113965

<400> 80

15

30

45

60

80

117/176

85

90

95

Lys Pro Arg Ala Trp Arg Gln Cys Gly Pro Gln Asn Gly Pro Arg Arg
 100 105 110

Ser Gln Ala Ile Thr Pro Glu Pro Gly Ala Ala Gly Arg His His Gln
 115 120 125

Pro Arg Gly Asp Arg Lys Pro Arg Ala Trp Arg Gln Cys Gly Pro Gln
 130 135 140

Asn Gly Pro Arg Arg Ser Gln Ala Ile Thr Pro Glu Pro Gly Ala Ala
 145 150 155 160

Gly Arg His His Gln Pro Arg Gly Asp Arg Lys Pro Arg Ala Trp Arg
 165 170 175

Gln Cys Gly Pro Gln Asn Gly Pro Arg Arg Ser Gln Ala Ile Thr Pro
 180 185 190

Glu Pro Gly Ala Ala Gly Arg His Trp Leu Asp Gln Arg Pro Val Val
 195 200 205

Pro Asp Gly Val Gly Lys Ser Asp Ser
 210 215

<210> 81
 <211> 27
 <212> PRT
 <213> M. tuberculosis

<220>
 <221> misc_feature
 <223> hypothetical protein Rv1572c

<220>
 <221> misc_feature
 <223> gi|2117265

<400> 81

His Gly Gln Pro Arg Thr Asn Thr Phe His His His Glu Lys Leu Leu
 1 5 10 15

Arg His Asn Asp Glu Asp Asn His Asp Asp Pro
 20 25

<210> 82

<211> 73
<212> PRT
<213> M. tuberculosis

<220>
<221> misc_feature
<223> hypothetical protein Rv0378

<220>
<221> misc_feature
<223> gi|2909499

<400> 82

Met Ser Gly Arg Trp Glu Ala Gly Asn Ala Asp Gly Asn Gly Gly Ser
1 5 10 15

Ala Gly Leu Ile Gly Ser Gly Gly Ala Gly Gly Asp Gly Gly Ser Gly
20 25 30

Gly Ala Thr Gly Ala Gly Gly Glu Gly Gly Asp Ala Gly Ala Ser Gly
35 40 45

Ser Ile Asn Gly Asn Ala Gly Asp Pro Gly Asn Ser Gly Glu Arg Gly
50 55 60

Ala Val Gly Lys Pro Gly Ala Pro Gly
65 70

<210> 83
<211> 47
<212> PRT
<213> N. meningitis MC58

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|7225315

<400> 83

Met Glu Trp Ala Glu Asn Glu Thr Val Lys Leu Ala Gln Lys Trp Glu
1 5 10 15

Gln Glu Gln Lys Lys Gln Gln Ile Gln Gln Lys Lys Glu Thr Glu Lys
20 25 30

Ser Pro Lys His Lys Ala Ser Arg Asp Asp Trp Glu Met Glu Arg
119/176

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35              40              45

<210>  84
<211>  107
<212>  PRT
<213>  N. meningitis MC58

<220>
<221>  misc_feature
<223>  hypothetical protein

<220>
<221>  misc_feature
<223>  gi|7226708

<400>  84

Met Lys Lys Leu Leu Ile Ala Ala Met Met Ala Ala Ala Leu Ala Ala
1              5              10              15

Cys Ser Gln Glu Ala Lys Gln Glu Val Lys Glu Ala Val Gln Ala Val
20              25              30

Glu Ser Asp Val Lys Asp Thr Ala Ala Ser Ala Ala Glu Ser Ala Ala
35              40              45

Ser Ala Val Glu Glu Ala Lys Asp Gln Val Lys Asp Ala Ala Ala Asp
50              55              60

Ala Lys Ala Ser Ala Glu Glu Ala Val Thr Glu Ala Lys Glu Ala Val
65              70              75              80

Thr Glu Ala Ala Lys Asp Thr Leu Asn Lys Ala Ala Asp Ala Thr Gln
85              90              95

Glu Ala Ala Asp Lys Met Lys Asp Ala Ala Lys
100              105

<210>  85
<211>  98
<212>  PRT
<213>  N. meningitis MC58

<220>
<221>  misc_feature
<223>  hypothetical protein

<220>
<221>  misc_feature
<223>  gi|7226768

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<400> 85

Met Lys Lys Ser Leu Phe Ala Ala Ala Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Ala Cys Gly Gly Glu Lys Ala Ala Glu Ala Pro Ala Ala Glu Ala Pro
20 25 30

Ala Ala Glu Ala Pro Ala Thr Glu Ala Pro Ala Ala Glu Ala Pro Ala
35 40 45

Ala Glu Ala Pro Ala Ala Glu Ala Pro Ala Ala Glu Ala Ala Ala Thr
50 55 60

Glu Ala Pro Ala Ala Glu Ala Ala Ala Thr Glu Ala Pro Ala Ala Glu
65 70 75 80

Ala Ala Ala Thr Glu Ala Pro Ala Ala Glu Ala Pro Ala Ala Glu Ala
85 90 95

Ala Lys

<210> 86

<211> 34

<212> PRT

<213> N. meningitis MC58

<220>

<221> misc_feature

<223> hypothetical protein

<220>

<221> misc_feature

<223> gi|7227030

<400> 86

Met Pro Trp Lys Ile Ser Thr Thr Thr Asn Leu Thr Pro Val Pro Ser
1 5 10 15

Ala Asn Leu Ser Ala Leu Pro Thr Thr Arg Cys Thr Thr Pro Pro Pro
20 25 30

Thr Pro

<210> 87

<211> 114
<212> PRT
<213> N. meningitis MC58

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|7227104

<400> 87

Met Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro
1 5 10 15

Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly
20 25 30

Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser
35 40 45

Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro
50 55 60

Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly
65 70 75 80

Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Pro
85 90 95

Ser Phe Pro Arg Arg Arg Glu Ser Arg Pro Val Gly Ala Glu Thr Tyr
100 105 110

Arg Val

<210> 88
<211> 120
<212> PRT
<213> N. meningitis MC58

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|7226645

<400> 88

Met Ile Ala Lys Ser Leu Phe Phe Arg Cys Gln Lys Ile Tyr Phe Ile
1 5 10 15

Tyr Phe Ile Leu Phe Ile Cys Leu Tyr Leu Asn Ile Ser Tyr Asp Gly
20 25 30

Glu Ile Phe Ile Tyr Phe Ile Ile Asn Phe Thr His Leu Leu Ile Cys
35 40 45

His Gly Ile Leu Leu Val Phe Cys Arg Ile Phe Pro Tyr Glu Asn Ile
50 55 60

Pro Phe Thr Ile Phe Leu Asn Phe Ile Ser Leu Phe Leu Ile Phe Leu
65 70 75 80

Pro Leu Ile Phe Thr Ile Arg Glu Leu Ile Asp Ser Tyr Tyr Ile Glu
85 90 95

Ser Ile Ile Asn Leu Phe Leu Ile Leu Ile Pro His Val Ile Phe Leu
100 105 110

Ile Tyr Leu Lys Gly Lys Gln Ile
115 120

<210> 89

<211> 78

<212> PRT

<213> Pseudomonas aeruginosa

<220>

<221> misc_feature

<223> AE004587_5 hypothetical protein

<220>

<221> misc_feature

<223> gi|9947556

<400> 89

Met Lys Lys Thr Val Thr Leu Ala Leu Leu Leu Ala Ala Ser Leu Gly
1 5 10 15

Leu Ala Ala Cys Asp Lys Lys Glu Glu Asp Lys Ala Ala Ala Pro Ala
20 25 30

Ala Pro Ala Thr Glu Thr Gln Pro Ser Ala Pro Ala Thr Pro Pro Ala
123/176

35

40

45

Glu Pro Ser Ala Pro Ala Pro Ser Ser Asp Thr Pro Ala Thr Pro Gln
 50 55 60

Thr Pro Ala Pro Thr Pro Glu Gln Pro Gln Gln Asn Gln Gln
 65 70 75

<210> 90
 <211> 52
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> misc_feature
 <223> AE004746_3 hypothetical protein

<220>
 <221> misc_feature
 <223> gi|9949353

<400> 90

Met Ser Leu Gly Thr Ile Leu Leu Ile Ile Leu Ile Leu Leu Leu Ile
 1 5 10 15

Gly Gly Leu Pro Val Phe Pro His Ser Arg Asn Trp Gly Tyr Gly Pro
 20 25 30

Ser Gly Ile Ile Gly Ala Leu Leu Val Val Leu Leu Val Leu Leu Leu
 35 40 45

Leu Gly Met Ile
 50

<210> 91
 <211> 126
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> misc_feature
 <223> AE004708_10 hypothetical protein

<220>
 <221> misc_feature
 <223> gi|9948900

<400> 91

Met Leu Lys Leu Phe Ala Thr Gly Leu Ala Ala Ser Phe Leu Leu Leu

1 5 10 15

Pro Pro Ala Gln Ala Ala Pro Pro Ala Pro Tyr Gly Val Gln Pro His
20 25 30

Gln Gln Ala Val Gln Arg Ala Gly Glu Gln Arg Gln Arg Gln Leu Gln
35 40 45

Glu Gln Arg Gln Arg Phe Asp Glu Gln Arg Leu Gln Leu Gln Gln Asp
50 55 60

Gln Leu Gln Arg Gln Gln Gln Asn Leu Gln Arg Gln Arg Gln Gln Arg
65 70 75 80

Gln Met Gln Asp Asn Leu Ile Arg Gln Gln Gln Leu Asp Gln Gln Arg
85 90 95

Trp Arg Leu Glu Gln Asp Gln Arg Arg Leu Asp Ser Glu Arg Arg Gln
100 105 110

Leu Glu Asn Arg Arg Arg Gln Ser Gln Ser Pro Ala Ile Arg
115 120 125

<210> 92
<211> 101
<212> PRT
<213> Pseudomonas aeruginosa

<220>
<221> misc_feature
<223> AE004643_2 hypothetical protein

<220>
<221> misc_feature
<223> gi|9948180

<400> 92

Met Ser Ala Asp Glu Lys Arg Ile Arg Glu Phe Ala Tyr Gln Ile Trp
1 5 10 15

Glu Ser Glu Gly Cys Pro Asp Gly Gln Ala Glu Arg His Trp Ala Met
20 25 30

Ala Arg Gln Leu Ala Glu Ala Glu Ala Ala Ala Ala Pro Lys Lys
35 40 45

Thr Arg Gly Arg Ala Lys Ala Ala Lys Glu Thr Pro Ala Leu Leu Gln
125/176

50

55

60

Ala Pro Ala Ala Lys Pro Arg Lys Pro Arg Ala Ala Ser Pro Ala Arg
65 70 75 80

Pro Ala Ser Glu Lys Pro Ala Ala Ala Lys Pro Arg Ser Arg Arg Lys
85 90 95

Pro Glu Ala Gly Glu
100

<210> 93
<211> 521
<212> PRT
<213> R. prowazekii

<220>
<221> misc_feature
<223> unknown

<220>
<221> misc_feature
<223> gi|3860652

<400> 93

Met Lys Lys Glu Ile Leu Ser Lys Gln Gly Asn Ile Leu Glu Gln Leu
1 5 10 15

Lys Phe Ile Asn Ala Asn Thr Glu Ile Leu Thr Glu His Ser Lys Ala
20 25 30

Ile Leu Lys Asp Lys Leu Lys Glu Leu Ser Lys Gln Leu Asp Glu Ile
35 40 45

Ser Ser Asn Lys Leu Val Gly Phe Ile Leu Asp Glu Asn Lys Ile Asn
50 55 60

Thr Asn Phe Lys Asn Val Pro Phe Ser Glu Lys Lys Val Arg Glu Gln
65 70 75 80

Val Asn Asn Leu Asn Asn Lys Ile Leu Glu Lys Ile Phe Leu Lys Asp
85 90 95

Asp Gly Thr Ile Thr Glu Gln Asp Leu Thr Lys Ile Leu Gln Lys His
100 105 110

Lys Glu Thr Val Leu Ile Lys Asn Leu Thr Lys Ala Ile Val Tyr Ile
126/176

115	120	125
Asp Gly Asn Lys Asn Asn Glu Thr Val Asn Lys Thr Leu Glu Lys Cys 130 135 140		
Leu Glu Glu Thr Thr Pro Glu Gln Gln Gly Met Ile Leu Asp Val Leu 145 150 155 160		
Thr Asn Asn Thr Arg Ile Arg Lys Ala Leu Ile Thr Lys Ile Glu Arg 165 170 175		
Glu Gln Arg Gln Glu His Asn Gln Lys Leu Asn Lys Asn Ile Ala Gly 180 185 190		
Asp Thr Phe Val Asp Ala Leu Lys Lys Ala Leu Val His Arg Thr Ser 195 200 205		
Asn Pro Glu Thr Ile Gln Lys Ser Leu Glu Arg Arg Lys Lys Glu Thr 210 215 220		
Pro Lys Asn Leu Asn Val Trp Asp Arg Ile Ser Gln Asn Ile Pro Asn 225 230 235 240		
Leu Asn Asn Gln Asn Asp Asn Gln Asn Gly Gln Asp Glu Asn Asn Lys 245 250 255		
Glu Trp Glu Glu Ser Asn Gln Asn Ala Asp Tyr Leu Asn Asn Thr Asn 260 265 270		
Ile Tyr Arg Ile Thr Lys Ala Lys Gln Asp Leu Glu Lys Ala Val Lys 275 280 285		
Glu Thr Ile Asn Lys Phe Ser Ala Met Ser Thr Leu Ile Lys Asp Asn 290 295 300		
Thr Ile Lys Asn Thr Met Ala Tyr Gln Lys Tyr Leu Lys Gly Ala Glu 305 310 315 320		
Asp Gln Leu Ala Leu Ala Lys Glu Lys Gly Lys Glu Leu Ile Glu Asn 325 330 335		
Ser Val Gln Thr Phe Lys Ile Ile Pro Lys Lys Tyr Gln Asp Asp Met 340 345 350		
Asn Glu Asn Trp Gln Asn Tyr Leu Ser Pro Glu Glu Ile Ile Glu Leu 127/176		

355		360		365
Thr Ala Leu Asn Glu His	Thr Asn Thr Leu Thr	Ser Asn Lys Asn Lys		
370	375	380		
Ser Gly Tyr Phe Thr	Ser Thr Ala Glu Ala	Leu Gln Cys Lys Thr	Lys	
385	390	395	400	
Gln Gln Glu Tyr Tyr	Thr Leu Leu Ser	Lys Leu Lys Lys	Ile Gly Ile	
405	410		415	
Glu Lys Gln Gln Lys	Lys Leu Val Lys	Asp Tyr Val Asp	Glu Met Ile	
420	425	430		
Thr Asn Ala Lys Gln	Ala Val Lys Lys	Ile Glu Arg Thr	Leu Glu Lys	
435	440	445		
Val Asn Gln Lys Lys	Glu Asn Lys Tyr	Glu Phe Ser Glu	Ser Ser Ala	
450	455	460		
Leu Ile Ser Lys Glu	Ile Leu Asp Ala	Gln Ala Arg Leu	Glu Asn Ala	
465	470	475	480	
Lys Gln Lys Ile Glu	Phe Ile Lys Leu	Lys Gln Ile Ile	Ser Asp Lys	
485	490	495		
Arg Gln Val Asn Ser	Ser Asp Glu Asp	Ser Asp Asp Asp	Ser Lys Lys	
500	505	510		
Lys Cys Asn Gln Thr	Lys Ser Arg Thr			
515	520			

<210> 94
 <211> 143
 <212> PRT
 <213> R. prowazekii

<220>
 <221> misc_feature
 <223> unknown

<220>
 <221> misc_feature
 <223> gi|3860651

<400> 94

Met Lys Ile Gln Met Met Ile Leu Lys Lys Asn Ala Ile Lys Leu Lys

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1	5	10	15												
Val	Glu	Leu	Glu	Asn	Ala	Gln	Lys	Asp	Ile	Asn	Gln	Ala	Lys	Lys	Asn
		20						25					30		
Leu	Glu	Asn	Ala	Glu	Ala	Lys	Asn	Glu	Ala	Leu	Gln	Arg	Gln	Ile	Ile
		35					40					45			
Leu	Asn	His	Asn	Gln	Asn	Glu	Val	Asn	Ser	His	Thr	Thr	Lys	Asn	Gln
	50					55					60				
Glu	Lys	Phe	Lys	Thr	Asp	Asn	Val	Thr	Glu	Glu	Tyr	Leu	Glu	Asp	Met
65					70					75					80
Ala	Leu	Met	Phe	Lys	Asn	Ser	Glu	Asp	Thr	Ala	Glu	Gln	Lys	Glu	Glu
				85					90					95	
Val	Asn	Cys	Gln	His	His	Glu	Glu	Gln	Asn	Arg	Gln	Lys	Gln	Glu	His
			100					105					110		
Ile	Asn	Thr	Glu	Glu	Glu	Ala	Val	His	Lys	Glu	Lys	Ile	Ile	His	Ile
		115					120					125			
Thr	Glu	Glu	Thr	Glu	Thr	Glu	Ala	Phe	Lys	Lys	Glu	Ile	Asp	Leu	
	130					135					140				

<210> 95
 <211> 369
 <212> PRT
 <213> T. pallidum

<220>
 <221> misc_feature
 <223> conserved hypothetical protein

<220>
 <221> misc_feature
 <223> gi|3322751

<400> 95

Met	Cys	Gln	Lys	Ser	Ser	Pro	Cys	Thr	Tyr	Ala	Arg	Val	Arg	Ser	Leu
1				5					10					15	

Pro	Ser	Val	Arg	Leu	Phe	Ser	Phe	Leu	Ala	Leu	Ala	Phe	Ala	Ser	Phe
			20					25					30		

Leu	Arg	Ala	Glu	Asp	Ala	Phe	Asp	His	Phe	Arg	Glu	Gly	Glu	Arg	Leu
129/176															

35					40					45					
Leu	Ser	Leu	Gln	Gln	Ala	Gln	Gln	Ala	Ile	Gly	Pro	Leu	His	Lys	Ala
50						55					60				
Ala	Gln	Gln	Lys	Pro	Ala	His	Pro	Lys	Ala	Ala	Leu	Tyr	Leu	Gly	Met
65					70					75					80
Ala	Tyr	Leu	Gln	Thr	Gly	Arg	Tyr	Thr	Gln	Ala	Ile	Gln	Trp	Leu	Gln
				85					90					95	
Asn	Pro	Pro	Val	His	Ser	Gln	Glu	Tyr	Ala	His	Leu	Tyr	Ala	Tyr	Asn
			100					105					110		
Leu	Gly	Asn	Val	Tyr	Phe	Val	Gln	His	Arg	Tyr	Glu	Glu	Ala	Gln	His
		115					120					125			
Ala	Tyr	Glu	Gln	Ala	Leu	Ala	Leu	Lys	His	Asp	Tyr	Pro	Pro	Ala	Leu
	130					135					140				
Leu	Asn	Arg	Ala	Asn	Thr	Ala	Met	Lys	Arg	Gln	Ala	Tyr	Ala	His	Ala
145					150					155					160
Leu	Ala	Asp	Tyr	Lys	Lys	Tyr	Val	Ser	Gln	Asn	Pro	Thr	Ala	Ser	Gln
				165					170					175	
His	Tyr	Glu	Val	Gln	Arg	Met	Ile	Ala	Ala	Leu	Glu	Gln	Trp	Leu	Gln
			180					185					190		
Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg	Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg
		195					200					205			
Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg	Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg
	210					215					220				
Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg	Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg
225					230					235					240
Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg	Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg
				245					250					255	
Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg	Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg
			260				265						270		
Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg	Arg	Lys	Glu	Ala	Glu	Glu	Ala	Arg

275	280	285
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg		
290	295	300
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg		
305	310	315 320
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Phe Glu Ala		
325	330	335
Leu Lys Arg Ala Leu Arg Leu Lys Gln Ala Glu Asp Ala Arg Thr Leu		
340	345	350
Ser Thr Gly Ser Glu Asp Thr Val Pro Tyr Gln Glu Glu His Asn Leu		
355	360	365

Glu

<210> 96
 <211> 41
 <212> PRT
 <213> T. pallidum

<220>
 <221> misc_feature
 <223> predicted coding region TP0266

<220>
 <221> misc_feature
 <223> gi|3322546

<400> 96

Met Val Arg Val Gln Arg Arg Val Leu Lys Asn Phe Met Arg Val Val
1 5 10 15

Gly Val Asp Lys Gly Tyr Arg Leu Trp Val Glu Trp Leu Ser Cys Val
20 25 30

Cys Cys Gly Tyr Val Val Arg Ala Glu
35 40

<210> 97
 <211> 38
 <212> PRT
 <213> Vibrio cholerae

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9654409

<400> 97

Met Ser Lys Gln Glu Met Lys Lys Pro Gln Leu Ser Leu Lys Glu Lys
1 5 10 15

Arg Lys Leu Lys Gln Glu Lys Ala Gln Glu Ser Ser Val Ile Lys Pro
20 25 30

Arg Lys Ser Lys Gly Arg
35

<210> 98
<211> 85
<212> PRT
<213> Vibrio cholerae

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9654544

<400> 98

Met Phe Leu Ser Phe Ile Cys Phe Tyr Ile Phe Lys Asn Gly Ser Tyr
1 5 10 15

Phe Ser Phe Ile Cys Leu Val Gly Cys Phe Gln Phe Phe Asp Phe Phe
20 25 30

Val Val Val Phe Ile Gly Phe Leu Phe Leu Phe Cys Ser Phe Gly Leu
35 40 45

Val Asp Phe Ser Phe Phe Tyr Phe Val Leu Ile Val Phe His Leu Phe
50 55 60

Gly Val Asp Leu Leu Ser Trp Phe Gly Trp Trp Gln Val Phe Leu Phe
65 70 75 80

Cys Asn Phe Ile Glu

<210> 99
 <211> 43
 <212> PRT
 <213> *Vibrio cholerae*

<220>
 <221> misc_feature
 <223> hypothetical protein

<220>
 <221> misc_feature
 <223> gi|9654912

<400> 99

Met Leu Asn His Leu Leu Val Arg Leu Thr Ile Gly Cys Leu Leu Val
 1 5 10 15

Leu Gly Ile Lys Leu Ser Ala Leu Tyr Phe Leu Pro Met Val Leu Leu
 20 25 30

Leu Asn Thr His His Lys Glu Phe Phe Gly Trp
 35 40

<210> 100
 <211> 31
 <212> PRT
 <213> *Vibrio cholerae*

<220>
 <221> misc_feature
 <223> hypothetical protein

<220>
 <221> misc_feature
 <223> gi|9656707

<400> 100

Met Pro Arg His Pro Phe Val Phe Val Val Ile Pro Lys Pro Pro Phe
 1 5 10 15

Leu Ala Val Val Ile Val Leu Arg Phe Val Val Thr Arg Tyr Leu
 20 25 30

<210> 101
 <211> 88
 <212> PRT
 <213> *Vibrio cholerae*

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9657609

<400> 101

Met Leu Ser Leu Ala Val Pro Leu Leu Phe Met Ser Leu Leu Gly Phe
1 5 10 15

Lys Leu Lys Leu Pro Tyr Gly Leu Leu Met Gly Leu Ile Ile Leu Thr
20 25 30

Leu Leu Leu Gly Trp Leu Gly Asn Val Ser Leu Leu Pro Val Leu Val
35 40 45

Val Leu Phe Phe Met Ser Pro Leu Leu Leu Ala Thr Lys Arg Ala Pro
50 55 60

Trp Gln Ser Ile Leu Phe Gly Val Gly Cys Leu Leu Pro Gln Leu Val
65 70 75 80

Gln Phe Val Met Leu Asn Gln Arg
85

<210> 102
<211> 33
<212> PRT
<213> Vibrio cholerae

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9657724

<400> 102

Met Arg Arg Leu Leu Cys Leu Ser Phe Asn Thr Leu His Leu Asn Gln
1 5 10 15

Ile Asn Asp Asn Gln Leu Lys Ser Leu Thr Lys Leu Arg Ile Ile Leu
20 25 30

Asn

<210> 103
<211> 34
<212> PRT
<213> *Vibrio cholerae*

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9657931

<400> 103

Met Gly Lys Ser Met Pro Ile Gln Leu Leu Leu Leu Ser Ile Pro Phe
1 5 10 15

Leu Leu Asp Ala Ala Thr Pro Ser Arg Leu Gly Ile Lys Ile Leu Ile
20 25 30

Leu Lys

<210> 104
<211> 36
<212> PRT
<213> *Vibrio cholerae*

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9658035

<400> 104

Met Gly Tyr Pro Ser Met Ala Ala Ala Leu His Ala Ala Ala Leu Asn
1 5 10 15

Ile Ala Leu Asn Ile Gln Leu Asn Ile Ser Met Arg Ala Met Leu Leu
20 25 30

Ala Phe Leu Glu
35

<210> 105

<211> 38
<212> PRT
<213> *Vibrio cholerae*

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9658254

<400> 105

Met Leu Ile Arg Glu Leu Ala Leu Ala Ala Tyr Gln Phe His Arg Tyr
1 5 10 15

Phe Lys Ile His Phe Met Phe Gln Phe Lys Val Phe Leu Phe Leu Ala
20 25 30

Lys Gly Phe Phe Ser Phe
35

<210> 106
<211> 35
<212> PRT
<213> *Vibrio cholerae*

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|9656580

<400> 106

Met Lys Leu Asn Asp Leu Asn Lys Lys Pro Leu Val Ile Lys Lys Thr
1 5 10 15

Ala Leu Ser Phe Gln Lys Leu Lys Lys Leu Gln Gln Pro Val Lys Lys
20 25 30

Phe His Phe
35

<210> 107
<211> 665
<212> PRT
<213> *Plasmodium falciparum*

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|3845248

<400> 107

Met Gln Tyr Phe Phe Leu Val Phe Leu Ala Val Leu Ala Lys Gly Phe
1 5 10 15

Leu Arg Asn Lys Glu His Ala Asn Leu Ile Asn Ser Tyr Asn Asp Ile
20 25 30

Val Glu Asp Ile Asn Ile Lys Lys Glu Glu Lys Ser Ser Ser Glu Pro
35 40 45

Pro Phe Ile Pro Ile Lys Asn Lys Ile Asp Asn Val His Thr Lys Asn
50 55 60

Asn Asn Gln Tyr Asn Leu His Asn Asn Lys Ser Asn Lys Thr His Leu
65 70 75 80

Thr Tyr Gly Thr His Thr Ser Phe Leu Gln Asn Cys Thr Ile Asn Asp
85 90 95

Cys Val Asp Val Asp Asn Lys Asp Ser Glu Ile Asn Asn Ile Thr Lys
100 105 110

Glu Lys Asp Asp Asn Asn Asn Asn Asn Gly Thr Lys Gln Ile Glu Glu
115 120 125

Lys Asn Lys Ile Asn Lys Ser Asp Leu His Arg Gln Asn Glu Leu Asn
130 135 140

Leu Gln Ser Gly Lys Asn Glu Gln Asp Ile Asn Lys Asn Glu Lys Gly
145 150 155 160

Lys Gln Asp Ile Ser Asn Ser Asn Ala Glu Asn Lys Lys Asp Val Lys
165 170 175

Glu Gly Val Lys Glu Leu Glu Glu Lys Lys Lys Glu Glu Lys Ile Ser
180 185 190

Asp Asp His Lys Val Glu Glu Asn Lys Lys Ser Asp Asp His Lys Val
137/176

195	200	205
Glu Glu Asn Lys Lys Ser Asp Asp His Lys Val Glu Glu Asn Lys Lys 210 215 220		
Ser Asp Asp His Lys Ile Glu Glu Val Lys Lys Val Glu Glu His Glu 225 230 235 240		
Glu Asp Glu Glu Glu Asp Lys Lys Glu Lys Lys Ser Glu Asn Lys Asn 245 250 255		
Lys Asp Glu Asn Lys Asp Glu Asn Asp Glu Asp Asn Asp Glu Ile Ser 260 265 270		
Asp Glu Asp Glu Val Asp Asp Asp Val Glu Glu Asp Lys Asn Glu Asn 275 280 285		
Asp Asp Ile Asp Asp Asp Lys Lys Glu Thr Asp Lys Thr His Leu Glu 290 295 300		
Glu Glu Glu Asn Glu Ile Ile Glu Lys Glu Phe Ser Asp Lys Lys Lys 305 310 315 320		
Asn Gly Lys Asn Lys Asp Thr Lys Lys Glu Lys Ser Lys Asp Thr Glu 325 330 335		
Lys Glu Lys Ser Lys Asp Ile Glu Lys Glu Lys Ser Lys Asp Lys Glu 340 345 350		
Lys Glu Lys Ser Lys Asp Lys Glu Lys Glu Lys Gly Lys Asp Lys Glu 355 360 365		
Lys Glu Lys Ser Lys Asp Ile Glu Lys Glu Lys Glu Lys Asp Lys Asp 370 375 380		
Ile Glu Lys Glu Lys Ser Lys Asp Thr Ala Lys Glu Lys Glu Lys Asp 385 390 395 400		
Lys Asp Ile Glu Lys Glu Lys Ser Lys Asp Met Glu Lys Leu Lys Asn 405 410 415		
Lys Gln Asn Asp Glu Lys Lys Lys Asp Asp Asn Glu Lys Lys Lys Asn 420 425 430		
Asp Lys Gln Asp Ile His Asp Asp Asn Asp Asp Glu Asn Asp Met Glu 138/176		

435	440	445
Glu Ile Glu Glu Asn Asp Asp Glu Glu Asp Glu Asp Glu Asp Met Glu 450 455 460		
Asn Lys Lys Lys Lys Lys Lys Gly Lys Asn Gly Asn Glu Asn Gly Asn 465 470 475 480		
Glu Asn Gly Ser Glu Asn Gly Asn Glu Asn Gly Asn Glu Asn Gly Asn 485 490 495		
Glu Asn Glu Asn Lys Asn Glu Ser Glu Asn Glu Asn Glu Asn Glu Asn 500 505 510		
Glu Asn Glu Asn Gly Asn Glu Asn Glu Asn Glu Lys Glu Asn Glu Lys 515 520 525		
Asp Lys Asn Ile Lys Glu Ile Glu Asn Val Thr Asn Ala Asn Lys Glu 530 535 540		
Asn Tyr Glu Lys Ile Asn Lys Asn Ser Glu Ile Thr Ile Thr Lys Ser 545 550 555 560		
Asn Ile Asp Ile Tyr Asn Asn Asn Arg Asn Asn Asp Ile Asp Lys Val 565 570 575		
Asn Asn His Ile Phe Thr Asn Gln Gln Lys Lys His Asn Leu His Asn 580 585 590		
Glu Gln Asn Lys Phe Asn Glu Thr Leu Asn Val Ser Thr Asn His Lys 595 600 605		
Asn His Tyr Glu Glu Lys Lys Lys Tyr Glu Ser Asn Met Phe Asn Val 610 615 620		
Asp Lys Arg Met His Lys Asn Leu Thr Ser Met Asp Thr Ile Leu His 625 630 635 640		
Asn Leu Asn Asp Lys Leu Ser His His Lys Asp Leu Lys Asn Val Leu 645 650 655		
Asn Asp Lys Lys Lys Lys Lys Asn Lys 660 665		

<210> 108

<211> 807
<212> PRT
<213> Plasmodium falciparum

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|3845292

<400> 108

Met Ala Val Glu Ser Lys Pro Asn Asn Ser Ser Lys Glu Lys Asn Glu
1 5 10 15

Glu Asn Asp Ile Ile Asn Lys Cys Asp Asp Ser Asn Lys Ile Asn Gly
20 25 30

Lys Glu Asn Ile Phe Ala Val Glu Lys Val Gly Ile Asn Glu Ser Gly
35 40 45

His Met Ser Asn Asp Asn Ile Asn Lys Asn Gln Glu Lys Asn Lys Lys
50 55 60

Lys Lys Lys Lys Lys Asn Thr His Lys Lys Val Asn Ile Asn Asn Thr
65 70 75 80

His Ile Asn Ile His Thr Thr Asn Asp Lys Asn Asn Gly Gln Asp Ile
85 90 95

Asn Lys Pro Glu Val Ile Glu Arg Asp Asn Ile Ile Asn Ile Lys Asn
100 105 110

Asp Thr Asn Asn Ile Leu Asp Ser Ser Tyr Asn Glu Glu Gly Asn Glu
115 120 125

Asn Asn Arg Asn Asp Ile Asn Asn Asn Asn Asn Asn Asn Ile Asn
130 135 140

Ile Asn Asn Asn Asn Ile Asn Asn Ser Cys Ser Asn Asn Tyr Gly Leu
145 150 155 160

Lys Lys Lys Ile Thr Leu Leu Lys Arg Asn Asp Ile Lys Asp Glu Gly
165 170 175

Tyr Asn Asn Glu Asn Ile Thr Thr Leu Asn Asn Lys Asn Asn Leu Lys
140/176

180				185				190							
Asn	Asn	Asn	Asn	Tyr	Asn	Asp	Asn	Arg	Asn	Asn	Asn	Asn	Asn	Asn	Lys
195				200				205							
Asn	Asn	Ile	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Cys	Cys	Ser	Glu	Lys	Thr
210		215				220									
Leu	Glu	Gln	Arg	Glu	Lys	Glu	Tyr	Asn	Lys	Ile	Arg	Ala	Arg	Ile	Phe
225		230				235				240					
Ser	Asn	Phe	Asn	Lys	Lys	Gln	Lys	Asn	Val	Gln	Lys	Thr	Glu	Gln	Asn
245				250				255							
Asn	Leu	Asn	His	Thr	Tyr	Leu	Asn	Asn	Asn	Ile	Ile	Asn	Asn	Ile	Asn
260				265				270							
Asn	Gly	Asp	Asn	Gln	Tyr	Ala	Tyr	Ile	Asn	Asn	Phe	Tyr	His	Ile	Tyr
275		280				285									
His	Asn	Asn	Ser	Tyr	Asn	His	Ile	Tyr	Arg	Gln	Asn	Asn	Ile	Pro	Ile
290		295				300									
Cys	Asn	Ile	Asn	Asn	His	Ala	Pro	Asn	Ile	Glu	Lys	Leu	Asn	Asn	Pro
305		310				315				320					
Tyr	Tyr	Tyr	His	Asp	Asn	His	Ile	Ala	Tyr	Thr	Asn	Tyr	Met	Tyr	Ser
325				330				335							
Thr	Gln	Asn	Lys	Met	Asn	Asn	Met	Lys	Thr	Lys	Gln	Ile	Gly	His	Tyr
340				345				350							
Gly	Ile	Asn	Asn	Glu	Asp	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Ile	Asn
355		360				365									
Asn	Asn	Asn	Asn	Asn	Asn	Ile	Asn	Asn	Asn	Asn	Ile	Asn	Asn	Asn	Asn
370		375				380									
Val	Pro	Leu	Cys	Ile	Pro	Gln	Leu	Asp	Asn	Tyr	Asn	Lys	Thr	Lys	Asn
385		390				395				400					
Asn	Phe	Asn	Gln	Gly	Thr	Asn	Asn	Phe	Asn	Gln	Gly	Thr	Asn	Asn	Phe
405				410				415							
Asn	Lys	Cys	Thr	Asn	Asn	Phe	Asn	Asn	Ala	Lys	Asn	His	Ile	Lys	His

420

425

430

Asn Ile Asn Asn Thr Asn Lys Asn Ile Glu His Leu Asn Asn His Ser
 435 440 445

Ile Tyr Asn Phe Val Tyr Pro Glu Asn Lys Asn Ile Tyr Asp Ala Asn
 450 455 460

Gly Asn Leu Ile Asn Asn Asn Ile Ser Tyr Thr Gln Leu Lys Met Asn
 465 470 475 480

Asn Asn Ile Asn Phe Asn Ile His Met Glu Ser Pro Ile Asn Gln Gln
 485 490 495

His Asn Asn Thr Phe Lys Val Asn Asn Asp Thr Asn Phe Phe Asn Glu
 500 505 510

Pro Thr Asn Lys Met Lys Lys Lys Asn Lys Glu Lys Lys Asn Ile His
 515 520 525

Phe Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Lys Cys Leu Tyr Lys Asp
 530 535 540

Ile Asn Gln Asn Asp His Asn Asn Ser Ile Ile Asn Thr Asn Gln Asn
 545 550 555 560

Phe Asp His Ile Asn Asn Val Lys Asn Thr Glu Gln Asn Leu Gln Lys
 565 570 575

Lys His Asn Lys Met Ser Gln Val Ser Lys Gln Ser Asn Asn Lys Asn
 580 585 590

Asn Lys Asn Asn Ser His Leu Lys Lys Gln Ile Asn Ile Asn Thr Asn
 595 600 605

Asn Asn Met Asp Asn Lys Asn Asn Ser His Ile Ser Lys Asn Val Ile
 610 615 620

Val Asp Asp Asn Lys Leu Lys Ser Ser His Ala Asp Asn Ser Asn Glu
 625 630 635 640

Ile Val Thr Lys Gly Lys Lys Lys Lys Asn Thr Asn Lys Lys Lys Lys
 645 650 655

Ile Asn Asn Ile Asn Ser Val Asn Asn Val Asn Asn Ile Asn Ser Met
 142/176

660

665

670

Asn Asn Ile Asn Ser Met Asn Asn Ile Ile Ser Met Asn Asn Val Asn
675 680 685

Asn Met Asn Asn Pro Met Tyr Phe Pro Asn Val Asn Ile Gln Lys Asp
690 695 700

Asp Ser Asn Ile Ala Leu Leu Tyr Asn Asn Lys Pro Asn Ile Asp Phe
705 710 715 720

Asn Asn Phe Gln Leu Asn His Ile Asn Asn His Met Ile Gln Asn Asn
725 730 735

Ile Met Thr Asn Asn Val Met Leu Asn Asn Asn Leu Thr Thr Ser Asn
740 745 750

Phe Asn Tyr Asn Leu Ile Asn Tyr Ser Tyr Glu Pro Phe Tyr Glu Glu
755 760 765

Asn Leu Met Asn Asp Leu Asp Tyr Cys Arg Asp Ile Ser Leu Tyr Glu
770 775 780

Lys Arg Tyr Asp Arg Gly Asp Asn Leu Gln Gln Asn His Lys Arg Tyr
785 790 795 800

Asp Ile Asp Phe Pro Ser Leu
805

<210> 109
<211> 861
<212> PRT
<213> Plasmodium falciparum

<220>
<221> misc_feature
<223> hypothetical protein

<220>
<221> misc_feature
<223> gi|4493994

<400> 109

Met Tyr Glu Leu Leu Leu Arg Phe Leu Lys Tyr Glu Cys Asp Tyr
1 5 10 15

Asp Asp Ser Glu Asp Ile Leu Asn Lys Tyr Cys Phe Ile Arg Glu Arg
143/176

20

25

30

Lys Tyr Asn Lys Pro Gly Gly Asn Lys Tyr Ile Pro Arg Asp Arg Ser
 35 40 45

Asn Asn Asn Asn Asn Ile Gly Asn Asn Val Asn Gly Met Asn Asn Phe
 50 55 60

Val Leu Leu Asn Asn Asn Asn Asn Met Arg Ile Arg Asn Thr Tyr
 65 70 75 80

Asn Asn Asn Asn Asn Asn Ile Asn Asn Asn Asn Asn Asn Asn Asn Asn
 85 90 95

Asn Phe Asn Asn Phe Asn Asn Asn Asn Asn Asn Asn Phe Asn Asn
 100 105 110

Phe Asn Asn Phe Asn Asn Asn Asn Asn Phe Asn Asn Asn Asn His Phe
 115 120 125

Asn Ile His Asn Ile Asp Asn Tyr Asp Asp Ser Tyr Val Lys Gly Arg
 130 135 140

His Arg Gly Asn Tyr Leu Ser Ser Ser Leu Asn Asn Ile Asn Gly Lys
 145 150 155 160

Val Phe Lys Asn Leu Asp Asp Asn Cys Tyr Asn Leu Pro Thr Asn Asn
 165 170 175

Leu Tyr Ile Asp Lys Glu Gly Lys Met His Leu Thr Gly Lys Glu His
 180 185 190

Tyr Asn Ala Ala Ser Ser Asn Glu Tyr Asn His Asn Asn Lys Asn Thr
 195 200 205

Asn Asn Tyr Asn Asn Asn Ser Tyr Asn Asn Asn Asn Phe Cys Asn Asn
 210 215 220

Asn Tyr Asn Asp Asn Asn Tyr Asn Asn Ser Asn Asn Lys Gly Met Gly
 225 230 235 240

Asn Lys Tyr Glu Arg Ser Leu Asn Tyr Leu Lys Lys Glu His Asp Met
 245 250 255

Val Asp Tyr Glu Tyr Asn Asn Lys Gly Asn Ile Arg Lys Asn Asp Ser

260

265

270

Glu Lys Tyr Trp Asp Asn Pro Pro Leu His Tyr Ser Lys Lys Asn Asn
 275 280 285

Tyr Asp Ile Phe Thr Leu Gly Asp Ile Lys Lys Tyr Ala Lys Asn Asn
 290 295 300

Glu Lys Lys Gly Asn Asn Lys Tyr Met Asn Met His Asp Asn Asn Ser
 305 310 315 320

Asn Asn Ser Asn Asn Val Leu Asn Asn Asn Asn Met Asn Ser Asn Ser
 325 330 335

Asn Asn Tyr Asn Asn Ile Phe Lys Asp Asn Asp Glu Glu Asn Leu Thr
 340 345 350

Lys Ser Asn Phe Ala Lys Trp Phe Lys Asn Asn Asn Asn Met Asn Val
 355 360 365

Asn Glu Asn Thr Asp Ile Ile Lys Tyr Leu Asn Asn Lys Asn Ser Gln
 370 375 380

Gly His Ser Asp Gly Lys Asn Asn Asn Asn Asn Asn Gly Asn Asn Ile
 385 390 395 400

Ile Asn Asn Asn Ser Asn Asn Lys Asn Asn Ile Phe Gln Gly Asn Ser
 405 410 415

Arg Asn Tyr Glu Asn Val Met Tyr Asn Ile Asn Asn Asn Asn Asn Asn
 420 425 430

Asn Ile Ile Ser Asn Asn Lys Asn Glu Ala Ser Phe Asn Thr Asp Asn
 435 440 445

Ile Asn Thr Asn Ser Gly Arg Glu Glu Glu Lys Ile Ser Asn Thr Val
 450 455 460

Ala Glu Leu Leu Met Lys Gln Ile Ser Met Ile Lys Glu Arg Asn Lys
 465 470 475 480

Gly Leu Asp Val Leu Glu Lys Lys Asn Thr Phe Gly Phe Leu Asp Asn
 485 490 495

Asn Tyr Gln Asn Tyr Gly Ser Asn Asn Asn Ser Ser Leu Glu Lys Asn
 145/176

500

505

510

Asn Met Lys Glu Asn Asp Ile Tyr Ser Lys Glu Ala Ser Lys Arg Ile
 515 520 525

Met Asp Ile Phe Arg Thr Leu Asn Ser Asn Gly Leu Val Ser Gln Glu
 530 535 540

Ser Leu Leu Val Asn Gln Ser Val Leu Asn Asn Asn Asn Tyr Asn
 545 550 555 560

Asn Tyr Asn Ser Asn Asn Asn Arg Asn Lys Asn Gln Asn Asn Asn Asn
 565 570 575

Asn Asn Asn Asn Asn Met Asn Asn Met Asn Asn Ser Asn Asn Asn Ile
 580 585 590

Asn Asn Asn Asn Asn Tyr Tyr Lys Asn Asn His Lys Tyr His Ser Met
 595 600 605

Asp Asn Val Thr Tyr Lys Lys Ile Phe Ile Asn Asn Tyr Ser Asn Asn
 610 615 620

Asp Gly Asn Asn Asn Ser Asn Asn Ser Asn Ser Asn Asn Asn Val Glu
 625 630 635 640

His Tyr Tyr Met Asn Asn Lys Lys Asn Phe Lys Asn Lys Ile Asn Asn
 645 650 655

Tyr His Asn Leu Pro Asp Asn Lys Asn Asn Met Met Asn Asn Asn Thr
 660 665 670

Tyr Asn Asn Ile Asn Lys Asn Asn Leu Ser Asn Met Glu Asn Phe Pro
 675 680 685

Pro Ser Leu Ser Phe Asn Asn Ser Asp Ile Asn Lys Asn Asn Ala Gln
 690 695 700

Gly Asn Ile Asn Ile Thr Pro Ile Ile Asn Ser Ile Leu Arg Leu Asp
 705 710 715 720

Asn Glu Val Asp Asn Val His Asn Asn Ser Ile Ser Glu Asn Ile Gln
 725 730 735

Asn Ala Lys Val Ser Asn Val Leu Asp Ser Leu Lys Ser Leu Leu Lys
 146/176

740

745

750

Ala Ser Lys Ser Gln Gly Asn Asn Asn Tyr Asn Ile Pro Lys Asn Phe
 755 760 765

Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Lys Phe Ile Asn Tyr Asn
 770 775 780

Ser Gln Gln Tyr Tyr Pro Ser His Gln Gln Gln Gln Gln Gln His Gln
 785 790 795 800

Gln Gln Gln Gln Gln Gln Gln Gln Gln Thr Leu Ile Gln Thr Gln Ile
 805 810 815

Asn Ser Thr His Leu Asn Asp Phe Asn Lys Lys Lys Phe Asn Lys Lys
 820 825 830

Glu Arg Tyr Pro Met Lys Tyr Pro Glu Phe Asp Gly Thr Thr Asn Glu
 835 840 845

Thr Met Met Val Arg Glu Lys Ala Glu Arg Gln Leu Val
 850 855 860

<210> 110
 <211> 54
 <212> PRT
 <213> Plasmodium falciparum

<220>
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 <223> Homologue of C.elegans F49C12.11 protein

<220>
 <221> misc_feature
 <223> gi|4494004

<400> 110

Met Pro Leu Asn Thr Gln Gly Gly Lys Lys Lys Pro Leu Lys Ala Ala
 1 5 10 15

Lys Lys Gly Pro Val Glu Leu Thr Glu Glu Asp Ile Ala Phe Lys Lys
 20 25 30

Glu Met Ala Glu Lys Lys Lys Ala Glu Glu Glu Ala Lys Gln Lys Leu
 35 40 45

Leu Lys Ala Lys Lys Lys

50

<210> 111
<211> 71
<212> PRT
<213> L. major

<220>
<221> misc_feature
<223> hypothetical protein P1105.01

<220>
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<223> gi|6996498

<400> 111

Met Arg Glu Arg Leu Ser Thr Asp Glu Tyr Val Tyr Trp Ser Gly Ile
1 5 10 15

Leu Leu Pro Leu Ile Arg Val Ile Asp Leu Ala Ser Val Asp Ser Pro
20 25 30

Leu Ala Leu Ala Leu Arg Ala Cys Val Cys Val Cys Val Cys Val Cys
35 40 45

Val Cys Val Cys Val Cys Val Cys Val Val Val Phe Leu Pro Leu Pro
50 55 60

Ser Leu Arg Ala Gln Ser Pro
65 70

<210> 112
<211> 923
<212> PRT
<213> L. major

<220>
<221> misc_feature
<223> AC005941_2 L5204.2

<220>
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<223> gi|6978417

<400> 112

Met Gln Leu Ser Gln Glu Asp Glu Glu Ala Ile Arg Thr Leu Arg Gly
1 5 10 15

Glu Ile Glu Ala Ala Trp Ala Lys Ala Asp Thr Ala His Glu Gln Glu

20

25

30

Gln Arg Ser Arg Glu Leu Leu His Thr Leu Arg Gln Gln Val Thr Glu
 35 40 45

Leu Asp Ala Met Val Glu Lys Thr Ala Gly Leu Ser Met Gly Gln Glu
 50 55 60

Ala Tyr Leu Arg Asp Leu Leu Thr Val Lys Lys Asp Arg Glu Glu Glu
 65 70 75 80

Ala Met Leu Leu His Ala Ala Leu Asn Arg Thr Glu Ala Asp His Arg
 85 90 95

Gln Val Cys Val Gln Leu Ala Ala Ala Lys Gln Ala His Glu Ala Ala
 100 105 110

Gln Arg Glu Arg Asp Glu Gln Arg Gln Val Tyr Gln His Leu Leu Thr
 115 120 125

Ser Leu Glu Ala Glu Gln Arg Glu Arg Ala Ala Lys Glu Ala Ser Val
 130 135 140

Arg Gln Tyr Arg Asp Thr Thr Glu Leu Cys Met Arg Arg Leu Asp Glu
 145 150 155 160

Arg Gly Val Glu Val Glu Arg Ala Ile Arg Glu Glu Lys Lys Ala Ala
 165 170 175

Lys Glu Ala Glu Gly Thr Ala Gln Glu Ile Gln Ala Ile Ala Arg Gln
 180 185 190

Leu Gln Glu Arg Gln Glu Arg Phe Gly Val Glu Ala Ala Arg Leu Ala
 195 200 205

Ala Ala Glu Arg Glu Asn Thr Ile Leu Thr Arg Glu Leu Pro Gln Arg
 210 215 220

Gln Ala Ala Leu His Glu Gln Gln Asp Glu Leu Lys Arg Glu Glu Lys
 225 230 235 240

Gln Leu His Leu Leu Glu Lys Ser Ala Arg Ala Gln Gln Ala Glu Leu
 245 250 255

Ala Ala Leu Val Glu Lys Arg Ala Thr Ala Ala Ala Ala Val Gln Thr
 149/176

260

265

270

Arg Ala Asn Ser Val Asp Ala Ala Leu Thr Glu Leu Ala Thr Glu Glu
 275 280 285

Lys Ala Arg Ala Ala Leu Glu Glu Ala Val Ala Lys Glu Met Gln Arg
 290 295 300

Lys Thr Asn Thr Met His Thr Asn Thr Phe Lys Ala Thr Ala Ser Ser
 305 310 315 320

Lys Val Glu Gly Gln Arg Val Met Glu Ala Gly Lys Ser Arg Arg Leu
 325 330 335

His Gln Gln Leu Glu Leu Leu Arg Thr Glu Asn Glu Lys Met Arg Lys
 340 345 350

Glu Ile Tyr Tyr Ala Glu Gln Asn His Glu Lys Asn Thr Lys Glu Ala
 355 360 365

Gln Gln Ala Leu Leu Asn Tyr His Arg Thr Leu Asp Ala Ile Arg Thr
 370 375 380

Arg Arg Ser Glu Ala Lys Ala Val Glu Glu Asp Ile Ala Leu His Gln
 385 390 395 400

Lys Lys Leu Lys Ala Gln Gln Ala Leu Leu Ser Thr Val Thr Ala Asp
 405 410 415

Arg Gln Lys Thr Glu Lys Ala Leu Arg Glu Thr Glu Ala Glu Leu Leu
 420 425 430

Leu Leu Arg Asn Arg His Ala Ser Lys Gln Glu Glu Leu Glu Ser Val
 435 440 445

Lys Thr Glu Leu Ile Gln Gln Glu Ala Asp Met Cys Gln Leu His Gly
 450 455 460

Leu Ser Arg Gln Leu Asn Lys Asp Val Ala Asn Thr Glu Gln Arg Leu
 465 470 475 480

Arg Phe Leu Arg Glu Asp Gln Gln His Ala Glu Ser Arg Val Glu Ala
 485 490 495

Leu Arg Ser Glu Ala Gln Glu Leu Arg Gln Val Ile Ala Gln Tyr Asp
 150/176

500					505					510					
Leu	Glu	Ala	Gln	Gln	Gln	Gly	Thr	Arg	Leu	Lys	Tyr	Met	Thr	His	Glu
		515					520					525			
Arg	Asn	Ala	Ile	Ala	Thr	Gln	Leu	Leu	Leu	Arg	Ser	Glu	Glu	Leu	Glu
	530					535					540				
Leu	Ile	Arg	Glu	Lys	Ile	Arg	Leu	Ala	Asp	Ala	Thr	Arg	Val	Ser	Gly
545					550				555						560
Thr	Thr	Lys	Tyr	Gln	Arg	Ala	Met	Lys	Gln	Leu	Leu	Glu	Ser	Arg	Asp
				565					570					575	
Leu	Leu	Val	Glu	Gln	Arg	Leu	Arg	Cys	Arg	Ile	Ala	Leu	Val	Arg	Leu
			580					585					590		
Arg	Tyr	Leu	Asp	Arg	Leu	His	Thr	Lys	Glu	Val	His	Gln	Glu	Lys	Leu
		595					600					605			
Leu	Ser	Gln	Ser	Arg	Ala	Arg	Val	Arg	Ala	Leu	Ala	Asp	Glu	Leu	Gly
	610					615					620				
Thr	Lys	His	Asn	Val	His	Cys	Trp	Arg	Ser	Met	Glu	Ser	Asn	Ala	Pro
625					630					635					640
Glu	Val	Leu	Asp	Ala	Leu	Ala	Lys	Val	Gln	Leu	Leu	Gln	Ala	Lys	Leu
				645					650					655	
Leu	Arg	Lys	His	Gly	Glu	Leu	Lys	Glu	Lys	Thr	Asp	Leu	Val	Glu	Lys
			660					665					670		
Glu	Glu	Arg	Ala	Tyr	Gln	Gln	Leu	Arg	Gln	Lys	Leu	Ala	Arg	Met	Pro
		675					680					685			
Gly	Pro	Glu	Ala	Ala	Glu	Glu	Leu	Ala	Leu	Cys	Ala	Glu	Asn	Met	Gln
	690					695					700				
Gln	Arg	Lys	Ala	Gln	Leu	Leu	Cys	Met	Thr	Asp	Ser	Leu	Ala	Glu	Ala
705				710						715					720
Glu	Gln	Glu	Ala	Glu	Val	Leu	Glu	Val	His	Val	Ala	Gln	Leu	Gln	Glu
				725					730					735	
Glu	Leu	Gln	Asp	Leu	Lys	His	Arg	Tyr	Tyr	Gln	Glu	Lys	Thr	Lys	His

740					745					750					
Ala	Ala	Leu	Arg	Gln	Glu	Glu	Lys	Leu	Val	Ala	Arg	Thr	Trp	Gly	Ala
		755					760					765			
Gly	Gly	Ala	Gly	Ala	Ala	Arg	Gln	Ala	Gly	Ser	Gly	Thr	Gly	Ser	Ser
		770					775					780			
Val	Gly	Asp	Gly	Asp	Gly	Ala	Val	Val	Ala	Ala	Gly	Ala	Ser	Ala	Pro
		785					790					795			800
Ser	Ala	Glu	Gln	Arg	Arg	Thr	Asn	Thr	Asp	Asp	Arg	Ser	Pro	Ser	Ala
				805					810					815	
Gly	Gly	Pro	Ala	Ser	Ala	Asp	Val	Glu	His	Arg	Ser	Ala	Ser	Gln	Pro
			820					825					830		
Gln	Gln	Pro	His	Ser	His	Ala	Gly	Gly	Ser	Ala	Ile	Val	Ser	Asn	Ser
		835					840					845			
His	Asn	Gly	Val	Gln	Ala	Ala	Ala	Ser	Gly	Thr	Gly	Arg	Met	Ser	Ala
		850					855					860			
Ala	Asn	Ser	Gly	Arg	Val	Gly	Asn	Gly	Ser	Val	Pro	Pro	Arg	Asn	Gly
				870								875			880
Arg	Arg	Arg	Ala	Pro	Leu	Ala	Glu	Ala	Ile	Leu	Asp	Thr	Leu	Thr	Ala
				885					890					895	
Gly	Pro	Pro	Gln	Pro	Asn	Phe	Pro	Leu	Gln	Arg	Pro	Pro	His	Gln	Arg
			900					905					910		
Gln	Phe	Val	Gly	Gly	Gly	Phe	Ser	Leu	Thr	Arg					
		915					920								

<210> 113
 <211> 2354
 <212> PRT
 <213> L. major

<220>
 <221> misc_feature
 <223> AC005802_5 L6202.3

<220>
 <221> misc_feature
 <223> gi|6899670

<400> 113

Met Ser Thr Pro Val Ser Gly Val Val Pro Gln Asp Arg Trp Gln Pro
1 5 10 15

Gln Gln Arg Val Lys Val Cys Gln Tyr Gln Asp Cys Gly Ala Pro Phe
20 25 30

Gly Phe Phe Ser Thr Lys Val Asn Cys His Arg Cys Gly Ile Val Leu
35 40 45

Cys Ser Lys Cys Ala Ala Thr Lys Thr Val Ile Pro Arg Tyr Tyr Ser
50 55 60

Asn Glu Thr Val Pro Val Cys Gln Arg Cys Tyr Gln Val Val Glu Arg
65 70 75 80

Tyr Lys Glu Arg Gly Ser Val Thr Pro Gly Tyr Val Val His Ser Thr
85 90 95

Thr Ile Ser Ala Thr Pro Ala Arg Ser Ser Pro Val Pro Pro Leu His
100 105 110

Thr Thr Pro Ala Leu Arg Pro His Ala Pro Ser Pro Gln Pro Ala Ser
115 120 125

Val Val Ser Thr Ala Thr Leu Val His Pro Val Glu Glu Asp Ala Val
130 135 140

Ser Thr Lys Pro Ser Val Ser Glu Ala Asp Leu His Ala Leu Arg Ser
145 150 155 160

Ile Ile Glu Thr Leu Gln Gln Ala Leu Asn Asp Glu Gln His Asn Ala
165 170 175

Ala Leu Ala Ala Thr Ser Ala Ala Glu Gln Leu Arg Thr Ala Lys Glu
180 185 190

Glu Asn Thr Ala Leu Lys Ser Thr Ala His Leu Leu Gln Gln Arg Leu
195 200 205

Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg
210 215 220

Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala
153/176

225		230		235		240
Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu						
		245		250		255
Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg						
		260		265		270
Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr						
		275		280		285
Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala						
		290		295		300
Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu						
305		310		315		320
Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu						
		325		330		335
Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln						
		340		345		350
Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr						
		355		360		365
Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp						
		370		375		380
Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln						
385		390		395		400
Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln						
		405		410		415
Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp						
		420		425		430
Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu						
		435		440		445
Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu						
		450		455		460
Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu						

465		470		475		480									
Glu	Ala	Arg	Val	Ala	Arg	Leu	Ala	Ala	Asp	Gly	Asp	Glu	Ala	Arg	Gln
				485					490					495	
Gln	Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr	Ala
			500					505					510		
Thr	Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Gln	Val	Ala	Arg	Leu	Ala	Ala
		515					520					525			
Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr	Ala	Thr	Gln	Gln	Arg
	530					535					540				
Ala	Glu	Leu	Glu	Ala	Arg	Val	Ala	Arg	Leu	Ala	Ala	Asp	Arg	Asp	Glu
545					550					555					560
Ala	Arg	Gln	Gln	Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu
				565					570					575	
Asp	Thr	Ala	Thr	Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Gln	Val	Ala	Arg
		580						585					590		
Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr	Ala	Thr
		595					600					605			
Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Arg	Val	Ala	Arg	Leu	Ala	Val	Asp
	610					615					620				
Arg	Asp	Glu	Ala	Arg	Gln	Gln	Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln
625					630					635					640
Gln	Arg	Leu	Asp	Thr	Ala	Thr	Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Gln
				645					650					655	
Val	Ala	Arg	Leu	Ala	Ala	Asp	Arg	Asp	Glu	Ala	Arg	Gln	Gln	Leu	Ala
			660					665					670		
Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr	Ala	Thr	Gln	Gln
		675					680					685			
Arg	Ala	Glu	Leu	Glu	Ala	Gln	Leu	Ala	Arg	Leu	Ala	Ala	Asp	Arg	Asp
	690					695					700				
Glu	Ala	Arg	Gln	Gln	Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg

705		710		715		720
Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala						
		725		730		735
Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn						
		740		745		750
Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala						
		755		760		765
Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala						
		770		775		780
Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp						
		785		790		795
Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu						
		805		810		815
Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu						
		820		825		830
Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu						
		835		840		845
Glu Ala Gln Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln						
		850		855		860
Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala						
		865		870		875
Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala						
		885		890		895
Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg						
		900		905		910
Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu						
		915		920		925
Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu						
		930		935		940
Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg						

945	950	955	960
Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala	965	970	975
Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu	980	985	990
Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg	995	1000	1005
Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp	1010	1015	1020
Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg	1025	1030	1035
Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn	1040	1045	1050
Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg	1055	1060	1065
Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp	1070	1075	1080
Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln	1085	1090	1095
Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln	1100	1105	1110
Val Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu	1115	1120	1125
Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr	1130	1135	1140
Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala	1145	1150	1155
Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu	1160	1165	1170
Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu	157/176		

1175	1180	1185
Glu Ala Gln Leu Ala Arg 1190	Leu Ala Ala Asp Arg 1195	Asp Glu Ala Arg 1200
Gln Gln Leu Ala Ala Asn 1205	Ala Glu Glu Leu Gln 1210	Gln Arg Leu Asp 1215
Thr Ala Thr Gln Gln Arg 1220	Ala Glu Leu Glu Ala 1225	Gln Val Ala Arg 1230
Leu Ala Ala Asp Gly Asp 1235	Glu Ala Arg Gln Gln 1240	Leu Ala Ala Asn 1245
Ala Glu Glu Leu Gln Gln 1250	Arg Leu Asp Thr Ala 1255	Thr Gln Gln Arg 1260
Ala Glu Leu Glu Ala Gln 1265	Leu Ala Arg Leu Ala 1270	Ala Asp Arg Asp 1275
Glu Ala Arg Gln Gln Leu 1280	Ala Ala Asn Ala Glu 1285	Glu Glu Leu Gln Gln 1290
Arg Leu Asp Thr Ala Thr 1295	Gln Gln Arg Ala Glu 1300	Leu Glu Ala Gln 1305
Val Ala Arg Leu Ala Ala 1310	Asn Ala Glu Glu Leu 1315	Gln Gln Arg Leu 1320
Asp Thr Ala Thr Gln Gln 1325	Arg Ala Glu Leu Glu 1330	Ala Arg Val Ala 1335
Arg Leu Ala Ala Asp Arg 1340	Asp Glu Ala Arg Gln 1345	Gln Leu Ala Ala 1350
Asn Ala Glu Glu Leu Gln 1355	Gln Arg Leu Asp Thr 1360	Ala Thr Gln Gln 1365
Arg Ala Glu Leu Glu Ala 1370	Arg Val Ala Arg Leu 1375	Ala Ala Asp Arg 1380
Asp Glu Ala Arg Gln Gln 1385	Leu Ala Ala Asn Ala 1390	Glu Glu Leu Gln 1395
Gln Arg Leu Asp Thr Ala 1400	Thr Gln Gln Arg Ala 1405	Glu Leu Glu Ala 1410

1400		1405		1410
Gln Val	Ala Arg Leu Ala	Ala Asn Ala Glu Glu	Leu	Gln Gln Arg
1415		1420		1425
Leu Asp	Thr Ala Thr Gln	Gln Arg Ala Glu Leu	Glu	Ala Arg Val
1430		1435		1440
Ala Arg	Leu Ala Ala Asp	Arg Asp Glu Ala Arg	Gln	Gln Leu Ala
1445		1450		1455
Ala Asn	Ala Glu Glu Leu	Gln Gln Arg Leu Asp	Thr	Ala Thr Gln
1460		1465		1470
Gln Arg	Ala Glu Leu Glu	Ala Gln Val Ala Arg	Leu	Ala Ala Asp
1475		1480		1485
Arg Asp	Glu Ala Arg Gln	Gln Leu Ala Ala Asn	Ala	Glu Glu Leu
1490		1495		1500
Gln Gln	Arg Leu Asp Thr	Ala Thr Gln Gln Arg	Ala	Glu Leu Glu
1505		1510		1515
Ala Arg	Val Ala Arg Leu	Ala Ala Asp Gly Asp	Glu	Ala Arg Gln
1520		1525		1530
Gln Leu	Ala Ala Asn Ala	Glu Glu Leu Gln Gln	Arg	Leu Asp Thr
1535		1540		1545
Ala Thr	Gln Gln Arg Ala	Glu Leu Glu Ala Gln	Leu	Ala Arg Leu
1550		1555		1560
Ala Ala	Asp Arg Asp Glu	Ala Arg Gln Gln Leu	Ala	Ala Asn Ala
1565		1570		1575
Glu Glu	Leu Gln Gln Arg	Leu Asp Thr Ala Thr	Gln	Gln Arg Ala
1580		1585		1590
Glu Leu	Glu Ala Arg Val	Ala Arg Leu Ala Ala	Asp	Gly Asp Glu
1595		1600		1605
Ala Arg	Gln Gln Leu Ala	Ala Asn Ala Glu Glu	Leu	Gln Gln Arg
1610		1615		1620
Leu Asp	Thr Ala Thr Gln	Gln Arg Ala Glu Leu	Glu	Ala Arg Val

1625	1630	1635
Ala Arg Leu Ala Ala Asp 1640	Arg Asp Glu Ala Arg 1645	Gln Gln Leu Ala 1650
Ala Asn Ala Glu Glu Leu 1655	Gln Arg Leu Asp 1660	Thr Ala Thr Gln 1665
Gln Arg Ala Glu Leu Glu 1670	Ala Gln Leu Ala Arg 1675	Leu Ala Ala Asp 1680
Arg Asp Glu Ala Arg Gln 1685	Gln Leu Ala Ala Asn 1690	Ala Glu Glu Leu 1695
Gln Gln Arg Leu Asp Thr 1700	Ala Thr Gln Gln Arg 1705	Ala Glu Leu Glu 1710
Ala Gln Leu Ala Arg Leu 1715	Ala Asp Gly Asp 1720	Glu Ala Arg Gln 1725
Gln Leu Ala Ala Asn Ala 1730	Glu Glu Leu Gln Gln 1735	Arg Leu Asp Thr 1740
Ala Thr Gln Gln Arg Ala 1745	Glu Leu Glu Val Glu 1750	Met Ala Val Leu 1755
Leu Arg Glu Arg Glu Glu 1760	Ala Arg Gly Glu Thr 1765	Ala Val Ala Gly 1770
Glu Gln Val Gln Leu Tyr 1775	Arg Glu Thr Val Glu 1780	Glu Glu Cys 1785
Leu Lys Glu Glu Arg Trp 1790	Cys Leu Glu Ser Arg 1795	Val Ala Gln Leu 1800
Arg Glu Ala Ser Ala Ala 1805	Ala Lys Gln Gln Arg 1810	Gln Glu Val Ala 1815
Ala Lys Ala Asn Glu Val 1820	Gln Glu Arg Leu Asp 1825	Ser Met Ala Arg 1830
Arg Cys Ile Ala His Glu 1835	Gly Asp Ala Pro Gln 1840	Arg Ala Asp Gly 1845
Arg Asp Asp Ala Leu Arg 1850	Gln Leu Ala Asn Leu Arg 1855	Glu Glu Val 1860

1850	1855	1860
Lys Leu Ser Glu Lys Gln 1865	Lys Ala Met Glu Arg 1870	Val Ile Pro Gly 1875
Val Arg Glu Arg Gln Met 1880	Arg Leu Glu Ala Ala 1885	Glu Glu Gln Arg 1890
Ala Asp Leu Glu Ala Arg 1895	Leu Val Asp Glu Ala 1900	Gly Asp Leu Arg 1905
Ser Arg Pro Ala Ala Ser 1910	Thr Asn Glu Val Asn 1915	Leu Tyr Arg Asp 1920
Leu Ala Leu Gln Glu His 1925	Glu Ala Ala Gln Asn 1930	Arg Cys Thr Thr 1935
Leu Glu Ala Gln Val Ala 1940	Ser Leu Thr Ser Asp 1945	Arg Asp Asn Gly 1950
Arg Gln Gln Glu Ser Ala 1955	Asp Leu Ser Glu Ala 1960	Gln Arg His Leu 1965
Asp Asn Val Gln Glu Arg 1970	Asp Met Ala His His 1975	Arg Cys Ala Ala 1980
Leu Glu Glu Gln Asn Ala 1985	Ala Met Ala Ser Glu 1990	Leu Gln Ala Val 1995
Lys Ala Lys Leu Arg Gln 2000	Ala Ser Val Lys Ala 2005	Ser Ser Leu Met 2010
Thr Arg Leu Ser Ala Ser 2015	Ser Ser Gly Ala Gly 2020	Gly Val Ser Ala 2025
Arg Val Arg Val Gly Gly 2030	Ser Ser Ala Val Pro 2035	Gln Ala Ala Pro 2040
His Arg Asp Ala Glu Leu 2045	Ile Ala Glu Val Gly 2050	Glu Arg Leu Arg 2055
Glu Arg Gly Glu Ala Met 2060	Arg Leu Leu Ala Glu 2065	Gly Val Glu Leu 2070
Arg Glu Arg Ala Arg Pro 2080	Leu Glu Arg Val Leu 2085	Ala Glu Lys Leu 2090

2075	2080	2085
Ile Gly Asp Arg Arg Thr Ser 2090	Asp Ala Glu Glu Val 2095	Ala Thr Glu 2100
Pro Thr Gln Val Arg Arg Asn 2105	Ala Ala His Ser Arg 2110	His Leu Asp 2115
Ser Arg Glu Ala Gln Leu Asp 2120	Glu Arg Ala Ala Arg 2125	Leu Arg Glu 2130
Lys Glu Gln Gln Leu Leu Arg 2135	Val Ala Arg Glu Leu 2140	Gln Thr Lys 2145
Ser Arg Ala Leu Gln Val Leu 2150	Tyr Ala Arg Ala Leu 2155	Asn Arg Pro 2160
Gln Val Thr Ser Leu Leu Leu 2165	Thr Ala Asp Gly Asp 2170	Asp Thr Ser 2175
Tyr Pro Asp Thr Pro Gln Gln 2180	Gln Gln Gln Gly Thr 2185	Arg Thr Pro 2190
Leu Arg Glu Pro Val Tyr Ser 2195	Leu Asp Ser Glu Val 2200	Ala His Tyr 2205
Gly Arg Thr Ala Gly Ala Ala 2210	Val Ser Ser Gly Leu 2215	Ala Ser Pro 2220
Leu Pro Arg Glu Pro Pro Arg 2225	Ala Arg Met Val His 2230	Arg Ala Val 2235
Glu Ala Thr Gly Thr Glu Glu 2240	Asp Thr Gln Val Arg 2245	Leu Thr Ala 2250
Ala Thr Glu Ala Tyr Arg Asp 2255	Val Leu Tyr Glu His 2260	Ile Leu Glu 2265
Ser Asn Gly Leu Gln Gly Val 2270	Asp Val Leu Ala Gln 2275	Tyr Leu Pro 2280
His His Thr Ser Gly Gly Gly 2285	Leu Lys Thr Pro Arg 2290	Leu Pro Gly 2295
Ser Gly Ile Ile Ser Lys Thr	Arg Ala Met Leu Arg	Ala Leu Glu

2300	2305	2310
Glu Arg Leu Gly Ala Ser Arg Gly Val Gly Arg Gly Val Asp Pro		
2315	2320	2325
Ala Val Gln Glu Arg Ser Leu Glu Ala Phe Arg Arg Leu Glu Ala		
2330	2335	2340
Ala Leu Ser Ala Leu Cys Gly Gly Ser His Ala		
2345	2350	

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<400> 114

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1 5 10 15
Gln Gln Arg Val Lys Val Cys Gln Tyr Gln Asp Cys Gly Ala Pro Phe
20 25 30
Gly Phe Phe Ser Thr Lys Val Asn Cys His Arg Cys Gly Ile Val Leu
35 40 45
Cys Ser Lys Cys Ala Ala Thr Lys Thr Val Ile Pro Arg Tyr Tyr Ser
50 55 60
Asn Glu Thr Val Pro Val Cys Gln Arg Cys Tyr Gln Val Val Glu Arg
65 70 75 80
Tyr Lys Glu Arg Gly Ser Val Thr Pro Gly Tyr Val Val His Ser Thr
85 90 95
Thr Ile Ser Ala Thr Pro Ala Arg Ser Ser Pro Val Pro Pro Leu His
100 105 110
Thr Thr Pro Ala Leu Arg Pro His Ala Pro Ser Pro Gln Pro Ala Ser

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115					120					125					
Val	Val	Ser	Thr	Ala	Thr	Leu	Val	His	Pro	Val	Glu	Glu	Asp	Ala	Val
130						135					140				
Ser	Thr	Lys	Pro	Ser	Val	Ser	Glu	Ala	Asp	Leu	His	Ala	Leu	Arg	Ser
145					150					155					160
Ile	Ile	Glu	Thr	Leu	Gln	Gln	Ala	Leu	Asn	Asp	Glu	Gln	His	Asn	Ala
				165					170					175	
Ala	Leu	Ala	Ala	Thr	Ser	Ala	Ala	Glu	Gln	Leu	Arg	Thr	Ala	Lys	Glu
			180					185					190		
Glu	Asn	Thr	Ala	Leu	Lys	Ser	Thr	Ala	His	Leu	Leu	Gln	Gln	Arg	Leu
		195					200					205			
Asp	Thr	Ala	Thr	Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Gln	Val	Ala	Arg
	210					215					220				
Leu	Ala	Ala	Asp	Arg	Asp	Glu	Ala	Arg	Gln	Gln	Leu	Ala	Ala	Asn	Ala
225					230					235					240
Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr	Ala	Thr	Gln	Gln	Arg	Ala	Glu
				245					250					255	
Leu	Glu	Ala	Arg	Val	Ala	Arg	Leu	Ala	Ala	Asp	Arg	Asp	Glu	Ala	Arg
			260					265					270		
Gln	Gln	Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr
		275					280					285			
Ala	Thr	Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Gln	Val	Ala	Arg	Leu	Ala
	290					295					300				
Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Thr	Ala	Thr	Gln	Gln
305					310					315				320	
Arg	Ala	Glu	Leu	Glu	Ala	Gln	Leu	Ala	Arg	Leu	Ala	Ala	Asp	Arg	Asp
				325					330					335	
Glu	Ala	Arg	Gln	Gln	Leu	Ala	Ala	Asn	Ala	Glu	Glu	Leu	Gln	Gln	Arg
			340					345					350		
Leu	Asp	Thr	Ala	Thr	Gln	Gln	Arg	Ala	Glu	Leu	Glu	Ala	Gln	Val	Ala

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355	360	365
Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 370 375 380		
Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala 385 390 395 400		
Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu 405 410 415		
Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala 420 425 430		
Gln Val Ala Arg Leu Ala Ala Asn Arg Asp Glu Ala Arg Gln Gln Leu 435 440 445		
Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln 450 455 460		
Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala Asp Arg 465 470 475 480		
Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 485 490 495		
Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val 500 505 510		
Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala 515 520 525		
Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 530 535 540		
Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asn Ala Glu Glu 545 550 555 560		
Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu 565 570 575		
Ala Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg 580 585 590		
Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala 165/176		

595	600	605
Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn 610 615 620		
Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala 625 630 635 640		
Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala 645 650 655		
Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 660 665 670		
Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu 675 680 685		
Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu 690 695 700		
Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu 705 710 715 720		
Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln 725 730 735		
Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 740 745 750		
Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala 755 760 765		
Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu 770 775 780		
Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala 785 790 795 800		
Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu 805 810 815		
Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln 820 825 830		
Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Gly 166/176		

835	840	845
Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 850 855 860		
Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val 865 870 875 880		
Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala 885 890 895		
Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 900 905 910		
Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu 915 920 925		
Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu 930 935 940		
Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 945 950 955 960		
Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala 965 970 975		
Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu 980 985 990		
Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg 995 1000 1005		
Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 1010 1015 1020		
Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 1025 1030 1035		
Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 1040 1045 1050		
Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala 1055 1060 1065		
Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu		

1070	1075	1080
Glu Leu Gln Gln Arg Leu Asp 1085	Thr Ala Thr Gln Gln 1090	Arg Ala Glu 1095
Leu Glu Ala Arg Val Ala Arg 1100	Leu Ala Ala Asn Ala 1105	Glu Glu Leu 1110
Gln Gln Arg Leu Asp Thr Ala 1115	Thr Gln Gln Arg Ala 1120	Glu Leu Glu 1125
Ala Gln Val Ala Arg Leu Ala 1130	Ala Asn Ala Glu Glu 1135	Leu Gln Gln 1140
Arg Leu Asp Thr Ala Thr Gln 1145	Gln Arg Ala Glu Leu 1150	Glu Ala Arg 1155
Val Ala Arg Leu Ala Ala Asp 1160	Arg Asp Glu Ala Arg 1165	Gln Gln Leu 1170
Ala Ala Asn Ala Glu Glu Leu 1175	Gln Gln Arg Leu Asp 1180	Thr Ala Thr 1185
Gln Gln Arg Ala Glu Leu Glu 1190	Ala Gln Val Ala Arg 1195	Leu Ala Ala 1200
Asn Ala Glu Glu Leu Gln Gln 1205	Arg Leu Asp Thr Ala 1210	Thr Gln Gln 1215
Arg Ala Glu Leu Glu Ala Gln 1220	Leu Ala Arg Leu Ala 1225	Ala Asp Arg 1230
Asp Glu Ala Arg Gln Gln Leu 1235	Ala Ala Asn Ala Glu 1240	Glu Leu Gln 1245
Gln Arg Leu Asp Thr Ala Thr 1250	Gln Gln Arg Ala Glu 1255	Leu Glu Ala 1260
Gln Val Ala Arg Leu Ala Ala 1265	Asn Ala Glu Glu Leu 1270	Gln Gln Arg 1275
Leu Asp Thr Ala Thr Gln Gln 1280	Arg Ala Glu Leu Glu 1285	Ala Arg Val 1290
Ala Arg Leu Ala Ala Asp Arg 1295	Asp Glu Ala Arg Gln 1300	Gln Leu Ala 1305

1295		1300		1305
Ala Asn 1310	Ala Glu Glu Leu 1310	Gln 1315	Gln Arg Leu Asp 1320	Thr Ala Thr Gln 1320
Gln Arg 1325	Ala Glu Leu Glu 1330	Ala 1330	Arg Val Ala Arg 1335	Leu Ala Ala Asp 1335
Gly Asp 1340	Glu Ala Arg Gln 1345	Gln 1345	Leu Ala Ala Asn 1350	Ala Glu Glu Leu 1350
Gln Gln 1355	Arg Leu Asp Thr 1360	Ala 1360	Thr Gln Gln Arg 1365	Ala Glu Leu Glu 1365
Ala Gln 1370	Val Ala Arg Leu 1375	Ala 1375	Ala Asn Ala Glu 1380	Glu Leu Gln Gln 1380
Arg Leu 1385	Asp Thr Ala Thr 1390	Gln 1390	Gln Arg Ala Glu 1395	Leu Glu Ala Arg 1395
Val Ala 1400	Arg Leu Ala Ala 1405	Asp 1405	Arg Asp Glu Ala 1410	Arg Gln Gln Leu 1410
Ala Ala 1415	Asn Ala Glu Glu 1420	Leu 1420	Gln Gln Arg Leu 1425	Asp Thr Ala Thr 1425
Gln Gln 1430	Arg Ala Glu Leu 1435	Glu 1435	Ala Gln Val Ala 1440	Arg Leu Ala Ala 1440
Asp Arg 1445	Asp Glu Ala Arg 1450	Gln 1450	Gln Leu Ala Ala 1455	Asn Ala Glu Glu 1455
Leu Gln 1460	Gln Arg Leu Asp 1465	Thr 1465	Ala Thr Gln Gln 1470	Arg Ala Glu Leu 1470
Glu Ala 1475	Arg Val Ala Arg 1480	Leu 1480	Ala Ala Asp Gly 1485	Asp Glu Ala Arg 1485
Gln Gln 1490	Leu Ala Ala Asn 1495	Ala 1495	Glu Glu Leu Gln 1500	Gln Arg Leu Asp 1500
Thr Ala 1505	Thr Gln Gln Arg 1510	Ala 1510	Glu Leu Glu Ala 1515	Gln Leu Ala Arg 1515
Leu Ala	Ala Asp Arg Asp 169/176	Glu	Ala Arg Gln Gln 169/176	Leu Ala Ala Asn 169/176

1520		1525		1530
Ala Glu Glu Leu Gln Gln Arg	Leu Asp Thr Ala Thr	Gln Gln Arg		
1535	1540	1545		
Ala Glu Leu Glu Ala Arg Val	Ala Arg Leu Ala Ala	Asp Gly Asp		
1550	1555	1560		
Glu Ala Arg Gln Gln Leu Ala	Ala Asn Ala Glu Glu	Leu Gln Gln		
1565	1570	1575		
Arg Leu Asp Thr Ala Thr Gln	Gln Arg Ala Glu Leu	Glu Ala Arg		
1580	1585	1590		
Val Ala Arg Leu Ala Ala Asp	Arg Asp Glu Ala Arg	Gln Gln Leu		
1595	1600	1605		
Ala Ala Asn Ala Glu Glu Leu	Gln Gln Arg Leu Asp	Thr Ala Thr		
1610	1615	1620		
Gln Gln Arg Ala Glu Leu Glu	Ala Gln Leu Ala Arg	Leu Ala Ala		
1625	1630	1635		
Asp Arg Asp Glu Ala Arg Gln	Gln Leu Ala Ala Asn	Ala Glu Glu		
1640	1645	1650		
Leu Gln Gln Arg Leu Asp Thr	Ala Thr Gln Gln Arg	Ala Glu Leu		
1655	1660	1665		
Glu Ala Gln Leu Ala Arg Leu	Ala Ala Asp Gly Asp	Glu Ala Arg		
1670	1675	1680		
Gln Gln Leu Ala Ala Asn Ala	Glu Glu Leu Gln Gln	Arg Leu Asp		
1685	1690	1695		
Thr Ala Thr Gln Gln Arg Ala	Glu Leu Glu Val Glu	Met Ala Val		
1700	1705	1710		
Leu Leu Arg Glu Arg Glu Glu	Ala Arg Gly Glu Thr	Ala Val Ala		
1715	1720	1725		
Gly Glu Gln Val Gln Leu Tyr	Arg Glu Thr Val Glu	Glu Glu Glu		
1730	1735	1740		
Cys Leu Lys Glu Glu Arg Trp	Cys Leu Glu Ser Arg	Val Ala Gln		
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1745	1750	1755
Leu Arg Glu Ala Ser Ala Ala 1760	Ala Lys Gln Gln Arg 1765	Gln Glu Val 1770
Ala Ala Lys Ala Asn Glu Val 1775	Gln Glu Arg Leu Asp 1780	Ser Met Ala 1785
Arg Arg Cys Ile Ala His Glu 1790	Gly Asp Ala Pro Gln 1795	Arg Ala Asp 1800
Gly Arg Asp Asp Ala Leu Arg 1805	Gln Leu Ala Asn Leu 1810	Arg Glu Glu 1815
Val Lys Leu Ser Glu Lys Gln 1820	Lys Ala Met Glu Arg 1825	Val Ile Pro 1830
Gly Val Arg Glu Arg Gln Met 1835	Arg Leu Glu Ala Ala 1840	Glu Glu Gln 1845
Arg Ala Asp Leu Glu Ala Arg 1850	Leu Val Asp Glu Ala 1855	Gly Asp Leu 1860
Arg Ser Arg Pro Ala Ala Ser 1865	Thr Asn Glu Val Asn 1870	Leu Tyr Arg 1875
Asp Leu Ala Leu Gln Glu His 1880	Glu Ala Ala Gln Asn 1885	Arg Cys Thr 1890
Thr Leu Glu Ala Gln Val Ala 1895	Ser Leu Thr Ser Asp 1900	Arg Asp Asn 1905
Gly Arg Gln Gln Glu Ser Ala 1910	Asp Leu Ser Glu Ala 1915	Gln Arg His 1920
Leu Asp Asn Val Gln Glu Arg 1925	Asp Met Ala His His 1930	Arg Cys Ala 1935
Ala Leu Glu Glu Gln Asn Ala 1940	Ala Met Ala Ser Glu 1945	Leu Gln Ala 1950
Val Lys Ala Lys Leu Arg Gln 1955	Ala Ser Val Lys Ala 1960	Ser Ser Leu 1965
Met Thr Arg Leu Ser Ala Ser	Ser Ser Gly Ala Gly	Gly Val Ser

1970	1975	1980
Ala Arg Val Arg Val Gly Gly Ser Ser Ala Val Pro Gln Ala Ala 1985 1990 1995		
Pro His Arg Asp Ala Glu Leu Ile Ala Glu Val Gly Glu Arg Leu 2000 2005 2010		
Arg Glu Arg Gly Glu Ala Met Arg Leu Leu Ala Glu Gly Val Glu 2015 2020 2025		
Leu Arg Glu Arg Ala Arg Pro Leu Glu Arg Val Leu Ala Glu Lys 2030 2035 2040		
Leu Ile Gly Asp Arg Arg Thr Ser Asp Ala Glu Glu Val Ala Thr 2045 2050 2055		
Glu Pro Thr Gln Val Arg Arg Asn Ala Ala His Ser Arg His Leu 2060 2065 2070		
Asp Ser Arg Glu Ala Gln Leu Asp Glu Arg Ala Ala Arg Leu Arg 2075 2080 2085		
Glu Lys Glu Gln Gln Leu Leu Arg Val Ala Arg Glu Leu Gln Thr 2090 2095 2100		
Lys Ser Arg Ala Leu Gln Val Leu Tyr Ala Arg Ala Leu Asn Arg 2105 2110 2115		
Pro Gln Val Thr Ser Leu Leu Leu Thr Ala Asp Gly Asp Asp Thr 2120 2125 2130		
Ser Tyr Pro Asp Thr Pro Gln Gln Gln Gln Gly Thr Arg Thr 2135 2140 2145		
Pro Leu Arg Glu Pro Val Tyr Ser Leu Asp Ser Glu Val Ala His 2150 2155 2160		
Tyr Gly Arg Thr Ala Gly Ala Ala Val Ser Ser Gly Leu Ala Ser 2165 2170 2175		
Pro Leu Pro Arg Glu Pro Pro Arg Ala Arg Met Val His Arg Ala 2180 2185 2190		
Val Glu Ala Thr Gly Thr Glu Glu Asp Thr Gln Val Arg Leu Thr		

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20 25 30

His Thr Asn Ser Phe Val Ser Gly Asp Val Phe His Val Trp Arg Val
35 40 45

Arg Ser Phe His Ser Ala Pro Ser Val Phe Phe Cys Phe Ser Val Cys
50 55 60

Thr His Leu Leu Phe Ser Pro Ser Ser Pro Tyr Ala His His Ala Arg
65 70 75 80

Val Cys Val Arg Ala Cys Val Cys Val Cys Val Cys Val Val
85 90

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Pro Leu Leu Lys His Tyr Ser Arg Gly Met Ala Ser Ser Gly Ser Ala
20 25 30

Lys Asp Asp Ala Leu Phe Leu Val Arg Arg Pro Lys Tyr Leu Val Ala
35 40 45

Gln Ala Val Asn Leu Ser Gly Ser Val Val Phe Phe His Ser Leu Arg
175/176

50

55

60

Glu Val Asp Val Ser Val Gly Ser Ile Val Val Asn Ser Leu Ala Phe
65 70 75 80

Val Ile Thr Val Leu Met Ser Val Leu Val Leu Arg Glu Gly Leu Leu
85 90 95

Arg Ala Arg Thr Thr Ala Gly Cys Leu Leu Val Met Val Gly Thr Ala
100 105 110

Leu Cys Thr Tyr Ser Ser Ser Ala Ser
115 120